

Search completed: January 5, 2006, 17:34:48
Job time : 9.84144 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:12:49 ; Search time 53.9112 Seconds
(without alignments)
1334.860 Million cell updates/sec

Title: US-10-734-472-2_COPY_330_431
Perfect score: 102
Sequence: 1 CKKHELYVSFRDLGWQDWII.....SSNVILKKYRNMVVVRACGCH 102

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	313	2	Q91403_CHICK	Q91403 gallus gall
2	102	100.0	398	2	Q9I8T6_CHICK	Q9i8t6 gallus gall
3	102	100.0	431	1	BMP7_HUMAN	P18075 homo sapien
4	80	78.4	108	2	Q8MJC0_SHEEP	Q8mjc0 ovis aries
5	59	57.8	141	2	O88684_RAT	O88684 rattus norv
6	59	57.8	430	1	BMP7_MOUSE	P23359 mus musculu
7	54	52.9	412	2	Q9BTB3_HUMAN	Q9btb3 homo sapien
8	54	52.9	446	2	Q4S5J3_TETNG	Q4s5j3 tetraodon n
9	53	52.0	306	2	Q9R228_RAT	Q9r228 rattus norv
10	49	48.0	49	2	Q9MZL9_CANFA	Q9mzl9 canis famil
11	46	45.1	365	2	Q5U916_PIG	Q5u916 sus scrofa
12	42	41.2	424	2	Q9YGH7_XENLA	Q9ygh7 xenopus lae

FILE 'MEDLINE, BIOSIS, BIOTECHDS, CAPLUS, EMBASE, USPATFULL' ENTERED AT
16:23:58 ON 06 JAN 2006

L1 43 S ((CHARETTE M) OR (CHARETTE, M))/AU
L2 31 DUP REM L1 (12 DUPLICATES REMOVED)
L3 1095930 S MEMORY
L4 4063 S OSTEOGENIC (W) PROTEIN (W) 1 OR OP-1
L5 6528 S OSTEOGENIC (W) PROTEIN (W) 1 OR OP-1 OR BMP-7 OR BONE(W) MORP
L6 975 S L3 AND L5
L7 314 S L6 AND HIPPOCAMP?
L8 314 DUP REM L7 (0 DUPLICATES REMOVED)
L9 332420 S CYSTEINE
L10 307 S L8 AND L9
L11 11097 S BONE(W) MORPHOGENETIC (W) PROTEIN (W) 2 OR BMP-2
L12 640 S L3 AND L11
L13 315981 S HIPPOCAMP?
L14 318 S L12 AND L13
L15 318 DUP REM L14 (0 DUPLICATES REMOVED)
L16 1598 S BONE (W) MORPHOGENETIC (W) PROTEIN (W) 5 OR BMP-5
L17 0 S L1 AND L16
L18 512 S L3 AND L16
L19 512 DUP REM L18 (0 DUPLICATES REMOVED)
L20 2381 S BONE (W) MORPHOGENETIC (W) PROTEIN (W) 6 OR BMP-6
L21 534 S L3 AND L20
L22 533 DUP REM L21 (1 DUPLICATE REMOVED)
L23 44 S 330-432
L24 0 S L8 AND L23
L25 162 S 330-431
L26 4 S L8 AND L25

FILE 'MEDLINE, BIOSIS, BIOTECHDS, CAPLUS, EMBASE, USPATFULL' ENTERED AT
16:41:20 ON 06 JAN 2006

L27 669 S L5 AND NEURON

L28 637 DUP REM L27 (32 DUPLICATES REMOVED)

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OM protein - protein search, using sw model

Run on: January 5, 2006, 16:58:38 ; Search time 188 Seconds
(without alignments)
1007.299 Million cell updates/sec

Title: US-10-734-472-2
Perfect score: 2292
Sequence: 1 MHVRSILRAAAPHSFVALWAP.....SSNVILKKYRNMVVRACGCH 431

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2292	100.0	431	2	AAR07335	Aar07335 Human Bon
2	2292	100.0	431	2	AAR12106	Aar12106 Mammalian
3	2292	100.0	431	2	AAR27289	Aar27289 Human ost
4	2292	100.0	431	2	AAR44746	Aar44746 Osteogeni
5	2292	100.0	431	2	AAR33408	Aar33408 Human OP-
6	2292	100.0	431	2	AAR54935	Aar54935 Osteogeni
7	2292	100.0	431	2	AAR46731	Aar46731 Human ost
8	2292	100.0	431	2	AAR50198	Aar50198 Human OP-

9	2292	100.0	431	2	AAR51644	Aar51644	hOP1 huma
10	2292	100.0	431	2	AAR60577	Aar60577	Osteogeni
11	2292	100.0	431	2	AAR47290	Aar47290	hOP1. 3/2
12	2292	100.0	431	2	AAR50236	Aar50236	Human OP-
13	2292	100.0	431	2	AAR57971	Aar57971	Human OP-
14	2292	100.0	431	2	AAR47250	Aar47250	hOP1. 3/2
15	2292	100.0	431	2	AAW00236	Aaw00236	Human ost
16	2292	100.0	431	2	AAR87537	Aar87537	Human ost
17	2292	100.0	431	2	AAR85757	Aar85757	hOP-1. 3/
18	2292	100.0	431	2	AAW16365	Aaw16365	Human hip
19	2292	100.0	431	2	AAW40190	Aaw40190	Human OP-
20	2292	100.0	431	2	AAW36853	Aaw36853	Full leng
21	2292	100.0	431	2	AAW27508	Aaw27508	Human ost
22	2292	100.0	431	2	AAW34783	Aaw34783	Human ost
23	2292	100.0	431	2	AAW53179	Aaw53179	Human ost
24	2292	100.0	431	2	AAW44302	Aaw44302	Human ost
25	2292	100.0	431	2	AAW71356	Aaw71356	Human ost
26	2292	100.0	431	2	AAW80749	Aaw80749	Human ost
27	2292	100.0	431	2	AAW59764	Aaw59764	Morphogen
28	2292	100.0	431	2	AAW17391	Aay17391	Human ost
29	2292	100.0	431	2	AAW86382	Aaw86382	Human ost
30	2292	100.0	431	2	AAW28656	Aay28656	Human ost
31	2292	100.0	431	2	AAW89679	Aaw89679	Human ost
32	2292	100.0	431	2	AAW95448	Aaw95448	Human ost
33	2292	100.0	431	2	AAW24093	Aay24093	Human ost
34	2292	100.0	431	2	AAW42797	Aay42797	Human ost
35	2292	100.0	431	2	AAW43108	Aay43108	Human ost
36	2292	100.0	431	2	AAW86339	Aaw86339	Human ost
37	2292	100.0	431	2	AAW18144	Aay18144	Human OP-
38	2292	100.0	431	3	AAW92587	Aay92587	Morphogen
39	2292	100.0	431	3	AAB09518	Aab09518	Human mor
40	2292	100.0	431	3	AAW92442	Aay92442	Human ost
41	2292	100.0	431	3	AAW82158	Aay82158	Human ost
42	2292	100.0	431	3	AAW57229	Aay57229	Human ost
43	2292	100.0	431	3	AAB02784	Aab02784	Human mor
44	2292	100.0	431	3	AAW97369	Aay97369	Human ost
45	2292	100.0	431	3	AAB08841	Aab08841	Amino aci

ALIGNMENTS

RESULT 1

AAR07335

ID AAR07335 standard; protein; 431 AA.

XX

AC AAR07335;

XX

DT 25-MAR-2003 (revised)

DT 30-JAN-1991 (first entry)

XX

DE Human Bone Morphogenesis Protein-7.

XX

KW human bone morphogenic protein-7; wound healing; tissue repair;

KW cartilage formation.

XX

OS Homo sapiens.

Search completed: January 5, 2006, 17:08:01
Job time : 192 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:04:33 ; Search time 45 Seconds
(without alignments)
791.849 Million cell updates/sec

Title: US-10-734-472-2
Perfect score: 2292
Sequence: 1 MHVRSRLRAAAPHSFVALWAP.....SSNVILKKYRNMVVRACGCH 431

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	2292	100.0	431	1	US-07-841-646-2	Sequence 2, Appli	
2	2292	100.0	431	1	US-07-901-703-2	Sequence 2, Appli	
3	2292	100.0	431	1	US-07-539-756-4	Sequence 4, Appli	
4	2292	100.0	431	1	US-08-147-023-2	Sequence 2, Appli	
5	2292	100.0	431	1	US-08-206-864-2	Sequence 2, Appli	
6	2292	100.0	431	1	US-08-278-729A-17	Sequence 17, Appli	
7	2292	100.0	431	1	US-08-480-528A-4	Sequence 4, Appli	
8	2292	100.0	431	1	US-08-479-666-4	Sequence 4, Appli	

9	2292	100.0	431	1	US-08-155-343A-17	Sequence 17, Appl
10	2292	100.0	431	1	US-08-406-672-17	Sequence 17, Appl
11	2292	100.0	431	1	US-08-643-563A-17	Sequence 17, Appl
12	2292	100.0	431	1	US-08-447-570-2	Sequence 2, Appli
13	2292	100.0	431	1	US-08-643-763A-17	Sequence 17, Appl
14	2292	100.0	431	1	US-08-462-623-17	Sequence 17, Appl
15	2292	100.0	431	1	US-08-451-953A-17	Sequence 17, Appl
16	2292	100.0	431	1	US-08-459-346-2	Sequence 2, Appli
17	2292	100.0	431	1	US-08-445-468A-17	Sequence 17, Appl
18	2292	100.0	431	1	US-08-901-200A-4	Sequence 4, Appli
19	2292	100.0	431	1	US-08-481-337A-10	Sequence 10, Appl
20	2292	100.0	431	1	US-08-449-700-2	Sequence 2, Appli
21	2292	100.0	431	1	US-07-989-847-6	Sequence 6, Appli
22	2292	100.0	431	1	US-08-449-699A-2	Sequence 2, Appli
23	2292	100.0	431	1	US-08-696-268B-4	Sequence 4, Appli
24	2292	100.0	431	1	US-08-461-397A-17	Sequence 17, Appl
25	2292	100.0	431	1	US-08-912-088-17	Sequence 17, Appl
26	2292	100.0	431	2	US-08-278-730A-17	Sequence 17, Appl
27	2292	100.0	431	2	US-08-458-811-2	Sequence 2, Appli
28	2292	100.0	431	2	US-08-889-419-2	Sequence 2, Appli
29	2292	100.0	431	2	US-08-445-467-17	Sequence 17, Appl
30	2292	100.0	431	2	US-08-480-515A-17	Sequence 17, Appl
31	2292	100.0	431	2	US-08-459-129-2	Sequence 2, Appli
32	2292	100.0	431	2	US-09-219-391-4	Sequence 4, Appli
33	2292	100.0	431	2	US-08-469-411-6	Sequence 6, Appli
34	2292	100.0	431	2	US-09-019-339B-2	Sequence 2, Appli
35	2292	100.0	431	2	US-09-170-936-17	Sequence 17, Appl
36	2292	100.0	431	2	US-08-402-542-2	Sequence 2, Appli
37	2292	100.0	431	2	US-08-461-113-17	Sequence 17, Appl
38	2292	100.0	431	2	US-08-828-281B-5	Sequence 5, Appli
39	2292	100.0	431	2	US-09-887-901-2	Sequence 2, Appli
40	2292	100.0	431	2	US-08-456-033-17	Sequence 17, Appl
41	2292	100.0	431	2	US-08-643-321-16	Sequence 16, Appl
42	2292	100.0	431	2	US-08-938-622-2	Sequence 2, Appli
43	2292	100.0	431	2	US-09-148-925C-2	Sequence 2, Appli
44	2292	100.0	431	2	US-08-957-425-2	Sequence 2, Appli
45	2292	100.0	431	2	US-09-780-601A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
 US-07-841-646-2
 ; Sequence 2, Application US/07841646
 ; Patent No. 5266683
 ; GENERAL INFORMATION:
 ; APPLICANT: OPPERMAN, HERMANN
 ; APPLICANT: OZKAYNAK, ENGIN
 ; APPLICANT: KUBERASAMPATH, THANGAVEL
 ; APPLICANT: RUEGER, DAVID C.
 ; APPLICANT: PANG, ROY H.L.
 ; TITLE OF INVENTION: OSTEOGENIC DEVICES
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
 ; STREET: 53 STATE STREET

Search completed: January 5, 2006, 17:13:33
Job time : 47 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:04:48 ; Search time 165 Seconds
(without alignments)
1091.421 Million cell updates/sec

Title: US-10-734-472-2
Perfect score: 2292
Sequence: 1 MHVRSRLRAAAPHSFVALWAP.....SSNVILKKYRNMVVRACGCH 431

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2292	100.0	431	2	US-08-822-186-2	Sequence 2, Appli
2	2292	100.0	431	2	US-08-937-755-2	Sequence 2, Appli
3	2292	100.0	431	2	US-08-957-425-2	Sequence 2, Appli
4	2292	100.0	431	2	US-08-260-675-17	Sequence 17, Appl
5	2292	100.0	431	3	US-09-045-331-2	Sequence 2, Appli
6	2292	100.0	431	3	US-09-828-607-2	Sequence 2, Appli
7	2292	100.0	431	3	US-09-887-901-2	Sequence 2, Appli
8	2292	100.0	431	3	US-09-982-543A-10	Sequence 10, Appl

9	2292	100.0	431	3	US-09-039-107-2	Sequence 2, Appli
10	2292	100.0	431	3	US-09-798-518-1	Sequence 1, Appli
11	2292	100.0	431	3	US-09-540-466-2	Sequence 2, Appli
12	2292	100.0	431	3	US-09-423-943-2	Sequence 2, Appli
13	2292	100.0	431	3	US-09-012-846-2	Sequence 2, Appli
14	2292	100.0	431	3	US-09-960-789-1	Sequence 1, Appli
15	2292	100.0	431	3	US-09-952-318A-17	Sequence 17, Appl
16	2292	100.0	431	4	US-10-062-370-5	Sequence 5, Appli
17	2292	100.0	431	4	US-10-083-825-2	Sequence 2, Appli
18	2292	100.0	431	4	US-10-122-026-2	Sequence 2, Appli
19	2292	100.0	431	4	US-10-272-503-2	Sequence 2, Appli
20	2292	100.0	431	4	US-10-050-050-17	Sequence 17, Appl
21	2292	100.0	431	4	US-10-286-152A-8	Sequence 8, Appli
22	2292	100.0	431	4	US-10-301-822-10	Sequence 10, Appl
23	2292	100.0	431	4	US-10-366-345-39	Sequence 39, Appl
24	2292	100.0	431	4	US-10-321-799-2	Sequence 2, Appli
25	2292	100.0	431	4	US-10-295-027-518	Sequence 518, App
26	2292	100.0	431	4	US-10-295-027-787	Sequence 787, App
27	2292	100.0	431	4	US-10-295-027-806	Sequence 806, App
28	2292	100.0	431	4	US-10-295-027-843	Sequence 843, App
29	2292	100.0	431	4	US-10-375-150-6	Sequence 6, Appli
30	2292	100.0	431	4	US-10-173-999-58	Sequence 58, Appl
31	2292	100.0	431	4	US-10-428-275-6	Sequence 6, Appli
32	2292	100.0	431	4	US-10-428-997A-2	Sequence 2, Appli
33	2292	100.0	431	4	US-10-302-812-28	Sequence 28, Appl
34	2292	100.0	431	4	US-10-290-554-1	Sequence 1, Appli
35	2292	100.0	431	4	US-10-753-916-2	Sequence 2, Appli
36	2292	100.0	431	5	US-10-806-852-2	Sequence 2, Appli
37	2292	100.0	431	5	US-10-995-979-2	Sequence 2, Appli
38	2292	100.0	431	5	US-10-865-514-17	Sequence 17, Appl
39	2292	100.0	431	5	US-10-492-380-8	Sequence 8, Appli
40	2292	100.0	431	5	US-10-917-265-4	Sequence 4, Appli
41	2292	100.0	431	5	US-10-968-791-5	Sequence 5, Appli
42	2292	100.0	431	6	US-11-016-499-1	Sequence 1, Appli
43	2292	100.0	431	6	US-11-021-902-1	Sequence 1, Appli
44	2292	100.0	431	6	US-11-021-984-16	Sequence 16, Appl
45	2292	100.0	431	6	US-11-098-889-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-08-822-186-2

; Sequence 2, Application US/08822186

; Publication No. US20010014662A1

; GENERAL INFORMATION:

; APPLICANT: RUEGER, David C.

; APPLICANT: TUCKER, Marjorie M.

; TITLE OF INVENTION: IMPROVED OSTEOGENIC DEVICES AND METHODS

; TITLE OF INVENTION: OF USE THEREOF FOR REPAIR OF ENDOCHONDRAL BONE AND

; TITLE OF INVENTION: OSTEOCHONDRAL DEFECTS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CREATIVE BIOMOLECULES, INC

; STREET: 45 SOUTH STREET

; CITY: HOPKINTON

Search completed: January 5, 2006, 17:16:25
Job time : 167 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:08:09 ; Search time 13 Seconds
(without alignments)
281.372 Million cell updates/sec

Title: US-10-734-472-2
Perfect score: 2292
Sequence: 1 MHVRSRLRAAAPHSFVALWAP.....SSNVILKKYRNMVVRACGCH 431

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 61072 seqs, 8486849 residues

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2292	100.0	431	6	US-10-816-768-39	Sequence 39, Appl
2	2292	100.0	431	6	US-10-650-326B-3	Sequence 3, Appli
3	2292	100.0	431	7	US-11-051-568-2	Sequence 2, Appli
4	2292	100.0	431	7	US-11-186-284-10	Sequence 10, Appl
5	2245	97.9	484	7	US-11-051-568-13	Sequence 13, Appl
6	2224.5	97.1	430	6	US-10-650-326B-19	Sequence 19, Appl

7	2224.5	97.1	430	7	US-11-051-568-25	Sequence 25, Appl
8	2057	89.7	408	7	US-11-051-568-15	Sequence 15, Appl
9	1479.5	64.6	454	6	US-10-650-326B-15	Sequence 15, Appl
10	1413.5	61.7	513	6	US-10-650-326B-16	Sequence 16, Appl
11	1409.5	61.5	513	7	US-11-000-463-816	Sequence 816, App
12	1399	61.0	317	7	US-11-051-568-11	Sequence 11, Appl
13	1337.5	58.4	438	6	US-10-650-326B-9	Sequence 9, Appli
14	1069.5	46.7	399	6	US-10-650-326B-23	Sequence 23, Appl
15	1069.5	46.7	399	7	US-11-051-568-27	Sequence 27, Appl
16	1031.5	45.0	402	6	US-10-650-326B-21	Sequence 21, Appl
17	1027.5	44.8	402	7	US-11-051-568-29	Sequence 29, Appl
18	752	32.8	139	6	US-10-650-326B-1	Sequence 1, Appli
19	740	32.3	139	6	US-10-650-326B-4	Sequence 4, Appli
20	729	31.8	139	6	US-10-816-768-68	Sequence 68, Appl
21	704	30.7	455	6	US-10-650-326B-14	Sequence 14, Appl
22	620	27.1	117	6	US-10-816-768-69	Sequence 69, Appl
23	591	25.8	169	7	US-11-051-568-9	Sequence 9, Appli
24	581	25.3	129	6	US-10-816-768-89	Sequence 89, Appl
25	572	25.0	102	6	US-10-816-768-55	Sequence 55, Appl
26	538	23.5	419	7	US-11-051-568-19	Sequence 19, Appl
27	536	23.4	396	7	US-11-051-568-5	Sequence 5, Appli
28	535	23.3	408	7	US-11-051-568-7	Sequence 7, Appli
29	519	22.6	102	6	US-10-816-768-52	Sequence 52, Appl
30	518	22.6	102	6	US-10-816-768-47	Sequence 47, Appl
31	512	22.3	97	6	US-10-650-326B-2	Sequence 2, Appli
32	508	22.2	102	6	US-10-816-768-53	Sequence 53, Appl
33	505.5	22.1	588	6	US-10-650-326B-7	Sequence 7, Appli
34	475.5	20.7	139	6	US-10-650-326B-5	Sequence 5, Appli
35	472.5	20.6	139	6	US-10-650-326B-6	Sequence 6, Appli
36	454	19.8	102	6	US-10-816-768-56	Sequence 56, Appl
37	414	18.1	102	6	US-10-816-768-57	Sequence 57, Appl
38	410	17.9	360	6	US-10-650-326B-8	Sequence 8, Appli
39	408	17.8	118	6	US-10-816-768-48	Sequence 48, Appl
40	400	17.5	102	7	US-11-051-568-30	Sequence 30, Appl
41	393.5	17.2	101	6	US-10-650-326B-29	Sequence 29, Appl
42	386.5	16.9	501	7	US-11-191-072-2	Sequence 2, Appli
43	372.5	16.3	101	6	US-10-816-768-49	Sequence 49, Appl
44	372.5	16.3	172	7	US-11-051-568-17	Sequence 17, Appl
45	370	16.1	102	6	US-10-816-768-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1

US-10-816-768-39

; Sequence 39, Application US/10816768

; Publication No. US20050250936A1

; GENERAL INFORMATION:

; APPLICANT: Oppermann, Hermann

; APPLICANT: Tai, Mei-Sheng

; APPLICANT: McCartney, John

; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins

; FILE REFERENCE: STK-075

; CURRENT APPLICATION NUMBER: US/10/816,768

; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 124

Search completed: January 5, 2006, 17:16:43
Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:00:43 ; Search time 40 Seconds
(without alignments)
1036.736 Million cell updates/sec

Title: US-10-734-472-2
Perfect score: 2292
Sequence: 1 MHVRS LR AA PHS F VAL WAP SSNVILKKYRN MVVRACGCH 431

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	
1	2292	100.0	431	1	BMHU7	bone morphogenetic	
2	2224.5	97.1	430	2	JQ1184	osteogenic protein	
3	1562	68.2	313	2	I51284	bone morphogenetic	
4	1484	64.7	452	2	I49542	bone morphogenetic	
5	1479.5	64.6	454	1	BMHU5	bone morphogenetic	
6	1413.5	61.7	513	1	BMHU6	bone morphogenetic	
7	1386.5	60.5	510	2	A54798	Vg-1-related prote	
8	1377	60.1	426	2	JH0690	bone morphogenetic	
9	1031.5	45.0	402	2	A45056	osteogenic protein	
10	987	43.1	187	2	PN0496	bone morphogenetic	

11	829	36.2	207	2	S37618	vgr protein - rat
12	783.5	34.2	461	2	S52408	SPDVR1 protein - s
13	704	30.7	455	2	A43918	TGF-beta-related p
14	584	25.5	398	2	JH0687	bone morphogenetic
15	581	25.3	398	2	JH0688	bone morphogenetic
16	557.5	24.3	393	2	S37073	bone morphogenetic
17	554.5	24.2	353	2	I50607	bone morphogenetic
18	544.5	23.8	394	2	S45355	bone morphogenetic
19	540	23.6	420	2	I49541	bone morphogenetic
20	538	23.5	408	2	S38343	bone morphogenetic
21	537	23.4	401	2	JH0689	bone morphogenetic
22	536	23.4	396	1	BMHU2	bone morphogenetic
23	535	23.3	408	1	BMHU4	bone morphogenetic
24	531	23.2	408	2	JH0801	bone morphogenetic
25	529	23.1	400	2	A49147	bone morphogenetic
26	529	23.1	405	2	I50608	bone morphogenetic
27	519	22.6	408	2	S58791	bone morphogenetic
28	504.5	22.0	588	2	A26158	decapentaplegic pr
29	411	17.9	351	2	A34201	bone morphogenetic
30	410	17.9	360	2	A29619	Vg1 embryonic grow
31	406	17.7	427	2	A40735	TGF beta homolog d
32	403.5	17.6	495	2	S43294	bone morphogenetic
33	402.5	17.6	365	2	T43286	cet-1 protein - Ca
34	400.5	17.5	501	2	A55452	cartilage-derived
35	397.5	17.3	501	2	JC2347	growth/differentia
36	355.5	15.5	413	2	JC4862	activin beta-A cha
37	354.5	15.5	366	2	A46607	growth/differentia
38	349	15.2	436	2	B55452	cartilage-derived
39	348.5	15.2	366	2	A45402	transforming growt
40	345.5	15.1	366	2	T03907	TGF-beta-related p
41	337	14.7	151	2	S43296	bone morphogenetic
42	334	14.6	125	2	S43295	bone morphogenetic
43	314.5	13.7	409	2	S01825	transforming growt
44	308	13.4	412	2	A36169	transforming growt
45	306.5	13.4	476	2	JC4646	bone morphogenetic

ALIGNMENTS

RESULT 1

BMHU7

bone morphogenetic protein 7 precursor - human

N;Alternate names: osteogenic protein 1

C;Species: Homo sapiens (man)

C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: C39263; S10529

R;Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozney, J.M.

Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990

A;Title: Identification of transforming growth factor beta family members present in bone-inductive protein purified from bovine bone.

A;Reference number: A39263; MUID:91088608; PMID:2263636

A;Accession: C39263

A;Molecule type: mRNA

A;Residues: 1-431 <CEL>

1	2292	100.0	431	1	BMP7_HUMAN	P18075	homo sapien
2	2229.5	97.3	430	1	BMP7_MOUSE	P23359	mus musculu
3	2026	88.4	412	2	Q9BTB3_HUMAN	Q9btb3	homo sapien
4	1922	83.9	398	2	Q9I8T6_CHICK	Q9i8t6	gallus gall
5	1903	83.0	424	2	Q6P4J4_XENTR	Q6p4j4	xenopus tro
6	1898	82.8	424	2	Q9YGH7_XENLA	Q9ygh7	xenopus lae
7	1881	82.1	365	2	Q5U916_PIG	Q5u916	sus scrofa
8	1738.5	75.9	446	2	Q4S5J3_TETNG	Q4s5j3	tetraodon n
9	1573	68.6	306	2	Q9R228_RAT	Q9r228	rattus norv
10	1562	68.2	313	2	Q91403_CHICK	Q91403	gallus gall
11	1508	65.8	453	2	P87373_CHICK	P87373	gallus gall
12	1496	65.3	432	2	Q9PTF9_BRARE	Q9ptf9	brachydanio
13	1484	64.7	452	1	BMP5_MOUSE	P49003	mus musculu
14	1483	64.7	454	2	Q8CCE0_MOUSE	Q8cce0	mus musculu
15	1479.5	64.6	454	1	BMP5_HUMAN	P22003	homo sapien
16	1463.5	63.9	446	2	Q7T288_BRARE	Q7t288	brachydanio
17	1427.5	62.3	450	2	Q4RQB0_TETNG	Q4rqb0	tetraodon n
18	1414.5	61.7	417	2	Q5CZV5_BRARE	Q5czv5	brachydanio
19	1413.5	61.7	483	2	Q4JCQ2_HUMAN	Q4j cq2	homo sapien
20	1413.5	61.7	513	1	BMP6_HUMAN	P22004	homo sapien
21	1413.5	61.7	513	2	Q5TCP3_HUMAN	Q5tcp3	homo sapien
22	1392.5	60.8	506	2	Q811S4_RAT	Q811s4	rattus norv
23	1386.5	60.5	510	1	BMP6_MOUSE	P20722	mus musculu
24	1386	60.5	441	2	Q52L10_XENLA	Q52l10	xenopus lae
25	1385	60.4	424	2	Q6F2B8_XENTR	Q6f2b8	xenopus tro
26	1380	60.2	426	2	Q6PF75_XENLA	Q6pf75	xenopus lae
27	1377	60.1	426	1	BMP7_XENLA	P30886	xenopus lae
28	1320.5	57.6	428	2	Q4VBA3_HUMAN	Q4vba3	homo sapien
29	1314.5	57.4	435	2	Q8BRW3_MOUSE	Q8brw3	mus musculu
30	1304.5	56.9	425	2	Q4SS30_TETNG	Q4ss30	tetraodon n
31	1154	50.3	318	2	Q5BN41_ONCMY	Q5bn41	oncorhynchu
32	1069.5	46.7	399	1	BMP8A_MOUSE	P34821	mus musculu
33	1061	46.3	206	2	Q95L63_RABIT	Q95l63	oryctolagus
34	1053	45.9	412	2	Q80VZ0_MOUSE	Q80vz0	mus musculu
35	1035.5	45.2	402	2	Q5T3A5_HUMAN	Q5t3a5	homo sapien
36	1035.5	45.2	402	2	Q7Z5Y6_HUMAN	Q7z5y6	homo sapien
37	1031.5	45.0	203	2	Q9CX35_MOUSE	Q9cx35	mus musculu
38	1031.5	45.0	402	1	BMP8B_HUMAN	P34820	homo sapien
39	1031.5	45.0	402	2	Q53ZM7_HUMAN	Q53zm7	homo sapien
40	987.5	43.1	399	2	Q8BNM2_MOUSE	Q8bnm2	mus musculu
41	987	43.1	187	1	BMP7_CANFA	P34819	canis famil
42	968.5	42.3	399	1	BMP8B_MOUSE	P55105	mus musculu
43	902	39.4	369	2	Q4SSG4_TETNG	Q4ssg4	tetraodon n
44	829	36.2	207	1	BMP6_RAT	Q04906	rattus norv
45	814.5	35.5	254	2	Q4THC3_TETNG	Q4thc3	tetraodon n

ALIGNMENTS

RESULT 1

BMP7_HUMAN

ID BMP7_HUMAN STANDARD; PRT; 431 AA.

AC P18075; Q9H512; Q9NTQ7;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Bone morphogenetic protein 7 precursor (BMP-7) (Osteogenic protein 1)
 DE (OP-1) (Eptotetermin alfa).
 GN Name=BMP7; Synonyms=OP1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=90291971; PubMed=2357959;
 RA Oezkaynak E., Rueger D.C., Drier E.A., Corbett C., Ridge R.J.,
 RA Sampath T.K., Oppermann H.;
 RT "OP-1 cDNA encodes an osteogenic protein in the TGF-beta family.";
 RL EMBO J. 9:2085-2093(1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91088608; PubMed=2263636;
 RA Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V.,
 RA Wang E.A., Wozney J.M.;
 RT "Identification of transforming growth factor beta family members
 RT present in bone-inductive protein purified from bovine bone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehvaeslaiho M.H., Liversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnell L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain;

OM protein - protein search, using sw model

Run on: January 5, 2006, 17:12:04 ; Search time 134.836 Seconds
(without alignments)
857.015 Million cell updates/sec

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Perfect score: 263
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	263	100.0	325	8	ADH17314	Adh17314 Human NOV
2	263	100.0	325	8	ADH17318	Adh17318 Human NOV
3	263	100.0	347	8	ADH17312	Adh17312 Human NOV
4	263	100.0	347	8	ADH17320	Adh17320 Human NOV
5	263	100.0	412	8	ABO84472	Abo84472 Human can
6	263	100.0	431	2	AAR07335	Aar07335 Human Bon
7	263	100.0	431	2	AAR12106	Aar12106 Mammalian
8	263	100.0	431	2	AAR27289	Aar27289 Human ost

9	263	100.0	431	2	AAR44746	Aar44746	Osteogeni
10	263	100.0	431	2	AAR33408	Aar33408	Human OP-
11	263	100.0	431	2	AAR54935	Aar54935	Osteogeni
12	263	100.0	431	2	AAR46731	Aar46731	Human ost
13	263	100.0	431	2	AAR50198	Aar50198	Human OP-
14	263	100.0	431	2	AAR51644	Aar51644	hOP1 huma
15	263	100.0	431	2	AAR60577	Aar60577	Osteogeni
16	263	100.0	431	2	AAR47290	Aar47290	hOP1. 3/2
17	263	100.0	431	2	AAR50236	Aar50236	Human OP-
18	263	100.0	431	2	AAR57971	Aar57971	Human OP-
19	263	100.0	431	2	AAR47250	Aar47250	hOP1. 3/2
20	263	100.0	431	2	AAW00236	Aaw00236	Human ost
21	263	100.0	431	2	AAR87537	Aar87537	Human ost
22	263	100.0	431	2	AAR85757	Aar85757	hOP-1. 3/
23	263	100.0	431	2	AAW16365	Aaw16365	Human hip
24	263	100.0	431	2	AAW40190	Aaw40190	Human OP-
25	263	100.0	431	2	AAW36853	Aaw36853	Full leng
26	263	100.0	431	2	AAW27508	Aaw27508	Human ost
27	263	100.0	431	2	AAW34783	Aaw34783	Human ost
28	263	100.0	431	2	AAW53179	Aaw53179	Human ost
29	263	100.0	431	2	AAW44302	Aaw44302	Human ost
30	263	100.0	431	2	AAW71356	Aaw71356	Human ost
31	263	100.0	431	2	AAW80749	Aaw80749	Human ost
32	263	100.0	431	2	AAW59764	Aaw59764	Morphogen
33	263	100.0	431	2	AAY17391	Aay17391	Human ost
34	263	100.0	431	2	AAW86382	Aaw86382	Human ost
35	263	100.0	431	2	AAY28656	Aay28656	Human ost
36	263	100.0	431	2	AAW89679	Aaw89679	Human ost
37	263	100.0	431	2	AAW95448	Aaw95448	Human ost
38	263	100.0	431	2	AAY24093	Aay24093	Human ost
39	263	100.0	431	2	AAY42797	Aay42797	Human ost
40	263	100.0	431	2	AAY43108	Aay43108	Human ost
41	263	100.0	431	2	AAW86339	Aaw86339	Human ost
42	263	100.0	431	2	AAY18144	Aay18144	Human OP-
43	263	100.0	431	3	AAY92587	Aay92587	Morphogen
44	263	100.0	431	3	AAB09598	Aab09598	Human OP-
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ALIGNMENTS

RESULT 1

ADH17314

ID ADH17314 standard; protein; 325 AA.

XX

AC ADH17314;

XX

DT 11-MAR-2004 (first entry)

XX

DE Human NOV1b protein - SEQ ID 4.

XX

KW NOVX; antidiabetic; anorectic; cardiant; hypotensive;

KW antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide;

KW protozoacide; nootropic; neuroprotective; antiparkinsonian;

KW anticonvulsant; osteopathic; antiarthritic; antiinflammatory;

KW dermatological; antiasthmatic; antilipaemic; metabolic; diabetes;

Search completed: January 5, 2006, 17:24:56
Job time : 135.836 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 5, 2006, 17:16:35 ; Search time 33.6395 Seconds
(without alignments)
646.373 Million cell updates/sec

Title: US-10-734-472-2_COPY_30_292
Perfect score: 263
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	263	100.0	431	1	US-07-841-646-2	Sequence 2, Appli
2	263	100.0	431	1	US-07-901-703-2	Sequence 2, Appli
3	263	100.0	431	1	US-07-539-756-4	Sequence 4, Appli
4	263	100.0	431	1	US-08-147-023-2	Sequence 2, Appli
5	263	100.0	431	1	US-08-206-864-2	Sequence 2, Appli
6	263	100.0	431	1	US-08-278-729A-17	Sequence 17, Appl
7	263	100.0	431	1	US-08-480-528A-4	Sequence 4, Appli
8	263	100.0	431	1	US-08-479-666-4	Sequence 4, Appli

9	263	100.0	431	1	US-08-155-343A-17	Sequence 17, Appl
10	263	100.0	431	1	US-08-406-672-17	Sequence 17, Appl
11	263	100.0	431	1	US-08-643-563A-17	Sequence 17, Appl
12	263	100.0	431	1	US-08-447-570-2	Sequence 2, Appli
13	263	100.0	431	1	US-08-643-763A-17	Sequence 17, Appl
14	263	100.0	431	1	US-08-462-623-17	Sequence 17, Appl
15	263	100.0	431	1	US-08-451-953A-17	Sequence 17, Appl
16	263	100.0	431	1	US-08-459-346-2	Sequence 2, Appli
17	263	100.0	431	1	US-08-445-468A-17	Sequence 17, Appl
18	263	100.0	431	1	US-08-901-200A-4	Sequence 4, Appli
19	263	100.0	431	1	US-08-481-337A-10	Sequence 10, Appl
20	263	100.0	431	1	US-08-449-700-2	Sequence 2, Appli
21	263	100.0	431	1	US-07-989-847-6	Sequence 6, Appli
22	263	100.0	431	1	US-08-449-699A-2	Sequence 2, Appli
23	263	100.0	431	1	US-08-696-268B-4	Sequence 4, Appli
24	263	100.0	431	1	US-08-461-397A-17	Sequence 17, Appl
25	263	100.0	431	1	US-08-912-088-17	Sequence 17, Appl
26	263	100.0	431	2	US-08-278-730A-17	Sequence 17, Appl
27	263	100.0	431	2	US-08-458-811-2	Sequence 2, Appli
28	263	100.0	431	2	US-08-889-419-2	Sequence 2, Appli
29	263	100.0	431	2	US-08-445-467-17	Sequence 17, Appl
30	263	100.0	431	2	US-08-480-515A-17	Sequence 17, Appl
31	263	100.0	431	2	US-08-459-129-2	Sequence 2, Appli
32	263	100.0	431	2	US-09-219-391-4	Sequence 4, Appli
33	263	100.0	431	2	US-08-469-411-6	Sequence 6, Appli
34	263	100.0	431	2	US-09-019-339B-2	Sequence 2, Appli
35	263	100.0	431	2	US-09-170-936-17	Sequence 17, Appl
36	263	100.0	431	2	US-08-402-542-2	Sequence 2, Appli
37	263	100.0	431	2	US-08-461-113-17	Sequence 17, Appl
38	263	100.0	431	2	US-08-828-281B-5	Sequence 5, Appli
39	263	100.0	431	2	US-09-887-901-2	Sequence 2, Appli
40	263	100.0	431	2	US-08-456-033-17	Sequence 17, Appl
41	263	100.0	431	2	US-08-643-321-16	Sequence 16, Appl
42	263	100.0	431	2	US-08-938-622-2	Sequence 2, Appli
43	263	100.0	431	2	US-09-148-925C-2	Sequence 2, Appli
44	263	100.0	431	2	US-08-957-425-2	Sequence 2, Appli
45	263	100.0	431	2	US-09-780-601A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
 US-07-841-646-2
 ; Sequence 2, Application US/07841646
 ; Patent No. 5266683
 ; GENERAL INFORMATION:
 ; APPLICANT: OPPERMAN, HERMANN
 ; APPLICANT: OZKAYNAK, ENGIN
 ; APPLICANT: KUBERASAMPATH, THANGAVEL
 ; APPLICANT: RUEGER, DAVID C.
 ; APPLICANT: PANG, ROY H.L.
 ; TITLE OF INVENTION: OSTEOGENIC DEVICES
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
 ; STREET: 53 STATE STREET

Search completed: January 5, 2006, 17:36:56
Job time : 34.6395 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:16:50 ; Search time 109.815 Seconds
(without alignments)
1000.675 Million cell updates/sec

Title: US-10-734-472-2_COPY_30_292
Perfect score: 263
Sequence: 1 DFSILDNEVHSSFIHRRRLRSQ.....KQPFMVAFKKATEVHFRSIR 263

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	263	100.0	325	4	US-10-428-275-8	Sequence 8, Appli	
3	263	100.0	347	4	US-10-428-275-2	Sequence 2, Appli	
4	263	100.0	347	4	US-10-428-275-10	Sequence 10, Appl	
5	263	100.0	408	4	US-10-367-094-173	Sequence 173, App	
6	263	100.0	427	4	US-10-367-094-171	Sequence 171, App	
7	263	100.0	427	4	US-10-367-094-175	Sequence 175, App	
8	263	100.0	431	2	US-08-822-186-2	Sequence 2, Appli	

9	263	100.0	431	2	US-08-937-755-2	Sequence 2, Appli
10	263	100.0	431	2	US-08-957-425-2	Sequence 2, Appli
11	263	100.0	431	2	US-08-260-675-17	Sequence 17, Appl
12	263	100.0	431	3	US-09-045-331-2	Sequence 2, Appli
13	263	100.0	431	3	US-09-828-607-2	Sequence 2, Appli
14	263	100.0	431	3	US-09-887-901-2	Sequence 2, Appli
15	263	100.0	431	3	US-09-982-543A-10	Sequence 10, Appl
16	263	100.0	431	3	US-09-039-107-2	Sequence 2, Appli
17	263	100.0	431	3	US-09-798-518-1	Sequence 1, Appli
18	263	100.0	431	3	US-09-540-466-2	Sequence 2, Appli
19	263	100.0	431	3	US-09-423-943-2	Sequence 2, Appli
20	263	100.0	431	3	US-09-012-846-2	Sequence 2, Appli
21	263	100.0	431	3	US-09-960-789-1	Sequence 1, Appli
22	263	100.0	431	3	US-09-952-318A-17	Sequence 17, Appl
23	263	100.0	431	4	US-10-062-370-5	Sequence 5, Appli
24	263	100.0	431	4	US-10-083-825-2	Sequence 2, Appli
25	263	100.0	431	4	US-10-122-026-2	Sequence 2, Appli
26	263	100.0	431	4	US-10-272-503-2	Sequence 2, Appli
27	263	100.0	431	4	US-10-050-050-17	Sequence 17, Appl
28	263	100.0	431	4	US-10-286-152A-8	Sequence 8, Appli
29	263	100.0	431	4	US-10-301-822-10	Sequence 10, Appl
30	263	100.0	431	4	US-10-366-345-39	Sequence 39, Appl
31	263	100.0	431	4	US-10-321-799-2	Sequence 2, Appli
32	263	100.0	431	4	US-10-295-027-518	Sequence 518, App
33	263	100.0	431	4	US-10-295-027-787	Sequence 787, App
34	263	100.0	431	4	US-10-295-027-806	Sequence 806, App
35	263	100.0	431	4	US-10-295-027-843	Sequence 843, App
36	263	100.0	431	4	US-10-375-150-6	Sequence 6, Appli
37	263	100.0	431	4	US-10-173-999-58	Sequence 58, Appl
38	263	100.0	431	4	US-10-428-275-6	Sequence 6, Appli
39	263	100.0	431	4	US-10-428-997A-2	Sequence 2, Appli
40	263	100.0	431	4	US-10-302-812-28	Sequence 28, Appl
41	263	100.0	431	4	US-10-290-554-1	Sequence 1, Appli
42	263	100.0	431	4	US-10-753-916-2	Sequence 2, Appli
43	263	100.0	431	5	US-10-806-852-2	Sequence 2, Appli
44	263	100.0	431	5	US-10-995-979-2	Sequence 2, Appli
45	263	100.0	431	5	US-10-865-514-17	Sequence 17, Appl

ALIGNMENTS

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RESULT 1
US-10-428-275-4
; Sequence 4, Application US/10428275
; Publication No. US20040067505A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-585
; CURRENT APPLICATION NUMBER: US/10/428,275
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: 09/966545
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/544511
; PRIOR FILING DATE: 2000-04-06

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Search completed: January 5, 2006, 17:43:37
Job time : 110.815 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:25:10 ; Search time 6.11628 Seconds
(without alignments)
364.935 Million cell updates/sec

Title: US-10-734-472-2_COPY_30_292
Perfect score: 263
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 61072 seqs, 8486849 residues

Word size : 0

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA_New:*
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4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	263	100.0	431	6	US-10-816-768-39	Sequence 39, Appl
2	263	100.0	431	6	US-10-650-326B-3	Sequence 3, Appli
3	263	100.0	431	7	US-11-051-568-2	Sequence 2, Appli
4	263	100.0	431	7	US-11-186-284-10	Sequence 10, Appl
5	195	74.1	408	7	US-11-051-568-15	Sequence 15, Appl
6	195	74.1	484	7	US-11-051-568-13	Sequence 13, Appl
7	120	45.6	317	7	US-11-051-568-11	Sequence 11, Appl

8	97	36.9	97	6	US-10-650-326B-2	Sequence 2, Appli
9	71	27.0	430	6	US-10-650-326B-19	Sequence 19, Appl
10	71	27.0	430	7	US-11-051-568-25	Sequence 25, Appl
11	16	6.1	454	6	US-10-650-326B-15	Sequence 15, Appl
12	13	4.9	399	6	US-10-650-326B-23	Sequence 23, Appl
13	13	4.9	399	7	US-11-051-568-27	Sequence 27, Appl
14	13	4.9	402	6	US-10-650-326B-21	Sequence 21, Appl
15	13	4.9	402	7	US-11-051-568-29	Sequence 29, Appl
16	13	4.9	438	6	US-10-650-326B-9	Sequence 9, Appli
17	13	4.9	513	6	US-10-650-326B-16	Sequence 16, Appl
18	13	4.9	513	7	US-11-000-463-816	Sequence 816, App
19	8	3.0	777	6	US-10-821-234-1658	Sequence 1658, Ap
20	7	2.7	489	6	US-10-467-657-7846	Sequence 7846, Ap
21	6	2.3	9	7	US-11-045-024-5201	Sequence 5201, Ap
22	6	2.3	9	7	US-11-045-024-5203	Sequence 5203, Ap
23	6	2.3	10	7	US-11-045-024-5231	Sequence 5231, Ap
24	6	2.3	10	7	US-11-045-024-5233	Sequence 5233, Ap
25	6	2.3	10	7	US-11-045-024-7199	Sequence 7199, Ap
26	6	2.3	10	7	US-11-045-024-7205	Sequence 7205, Ap
27	6	2.3	11	7	US-11-045-024-5709	Sequence 5709, Ap
28	6	2.3	15	7	US-11-106-932-65	Sequence 65, Appl
29	6	2.3	15	7	US-11-106-932-83	Sequence 83, Appl
30	6	2.3	15	7	US-11-045-024-13058	Sequence 13058, A
31	6	2.3	16	7	US-11-106-932-52	Sequence 52, Appl
32	6	2.3	30	7	US-11-106-932-9	Sequence 9, Appli
33	6	2.3	30	7	US-11-106-932-18	Sequence 18, Appl
34	6	2.3	31	7	US-11-106-932-2	Sequence 2, Appli
35	6	2.3	48	7	US-11-000-463-304	Sequence 304, App
36	6	2.3	48	7	US-11-000-463-776	Sequence 776, App
37	6	2.3	106	7	US-11-020-772-20	Sequence 20, Appl
38	6	2.3	112	6	US-10-485-788A-787	Sequence 787, App
39	6	2.3	112	7	US-11-053-076-169	Sequence 169, App
40	6	2.3	154	7	US-11-082-389-424	Sequence 424, App
41	6	2.3	163	7	US-11-102-240-160	Sequence 160, App
42	6	2.3	220	6	US-10-995-561-976	Sequence 976, App
43	6	2.3	222	6	US-10-793-626-376	Sequence 376, App
44	6	2.3	257	6	US-10-118-590-16	Sequence 16, Appl
45	6	2.3	261	7	US-11-102-240-118	Sequence 118, App

ALIGNMENTS

RESULT 1

US-10-816-768-39

; Sequence 39, Application US/10816768

; Publication No. US20050250936A1

; GENERAL INFORMATION:

; APPLICANT: Oppermann, Hermann

; APPLICANT: Tai, Mei-Sheng

; APPLICANT: McCartney, John

; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins

; FILE REFERENCE: STK-075

; CURRENT APPLICATION NUMBER: US/10/816,768

; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 124

; SOFTWARE: PatentIn version 2.0

; REGISTRATION NUMBER: 43,153
; REFERENCE/DOCKET NUMBER: STK-001CP6C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-11-051-568-29

Query Match 4.9%; Score 13; DB 7; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 137 GEAVTAAEFRIYK 149
 |||||||
Db 138 GEAVTAAEFRIYK 150

Search completed: January 5, 2006, 17:44:05
Job time : 7.11628 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:13:39 ; Search time 22.797 Seconds
(without alignments)
1110.013 Million cell updates/sec

Title: US-10-734-472-2_COPY_30_292
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	71	27.0	430	2	JQ1184	osteogenic protein	
4	28	10.6	313	2	I51284	bone morphogenetic	
5	16	6.1	452	2	I49542	bone morphogenetic	
6	16	6.1	454	1	BMHU5	bone morphogenetic	
7	13	4.9	402	2	A45056	osteogenic protein	
8	13	4.9	510	2	A54798	Vg-1-related prote	
9	13	4.9	513	1	BMHU6	bone morphogenetic	
10	11	4.2	426	2	JH0690	bone morphogenetic	

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ILSILGLP 36
|||||||
Db 102 ILSILGLP 109

RESULT 14

AD1066

hypothetical protein STY4858 [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi (strain CT18)

C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

A;Note: this species has also been called *Salmonella typhi*

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AD1066

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebaihia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.

A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AD1066

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-202 <PAR>

A;Cross-references: UNIPARC:UPI000005A9AC; GB:AL513382; PIDN:CAD03347.1;

PID:g16505619; GSPDB:GN00176

C;Genetics:

A;Gene: STY4858

Query Match 3.0%; Score 8; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 LQLSVETL 223
|||||||
Db 184 LQLSVETL 191

RESULT 15

T39619

ubiquinol-cytochrome-c reductase (EC 1.10.2.2) Rieske iron-sulfur protein [similarity] - fission yeast (*Schizosaccharomyces pombe*)

C;Species: *Schizosaccharomyces pombe*

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T39619

R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M. submitted to the EMBL Data Library, March 1998

A;Reference number: Z21843

A;Accession: T39619

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
 A;Residues: 1-228 <WOO>
 A;Cross-references: UNIPROT:Q09154; UNIPARC:UPI0000137A6F; EMBL:AL022104;
 PIDN:CAA17904.1; GSPDB:GN00067; SPDB:SPBC16H5.06
 A;Experimental source: strain 972h-; cosmid c16H5
 C;Genetics:
 A;Gene: SPDB:SPBC16H5.06
 A;Map position: 2
 C;Superfamily: ubiquinol-cytochrome-c reductase (cytochrome c1) (complex III),
 iron-sulfur subunit; Rieske [2Fe-2S] homology
 C;Keywords: 2Fe-2S; metalloprotein; oxidoreductase; Rieske iron-sulfur protein
 F;172,174,191,194/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent)
 #status predicted
 F;177-193/Disulfide bonds: #status predicted
 F;194/Active site: His #status predicted

Query Match 3.0%; Score 8; DB 2; Length 228;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 DLSKIPEG 137
 |||||
 Db 110 DLSKIPEG 117

OM protein - protein search, using sw model

Run on: January 5, 2006, 17:12:04 ; Search time 19.9947 Seconds
(without alignments)
857.015 Million cell updates/sec

Title: US-10-734-472-2_COPY_292_330
Perfect score: 39
Sequence: 1 RSTGSKQRSQNRSKTPKNQEALRMANVAENSSSDQRQAC 39

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	100.0	317	2	AAR44750	Aar44750 Osteogeni
2	39	100.0	317	2	AAR51656	Aar51656 Osteogeni
3	39	100.0	317	2	AAR85766	Aar85766 OPlB fusi
4	39	100.0	317	2	AAW44306	Aaw44306 Human ost
5	39	100.0	317	2	AAW89683	Aaw89683 Osteogeni
6	39	100.0	317	2	AAY43117	Aay43117 Osteogeni
7	39	100.0	317	7	ADJ62686	Adj62686 Human ost
8	39	100.0	317	8	ADE52757	Ade52757 Human ost

9	39	100.0	317	8	ADM80495	Adm80495 Human ost
10	39	100.0	317	8	ADO03617	Ado03617 Human ost
11	39	100.0	408	2	AAR44752	Aar44752 Osteogeni
12	39	100.0	408	2	AAR51658	Aar51658 Osteogeni
13	39	100.0	408	2	AAR85768	Aar85768 OP1D fusi
14	39	100.0	408	2	AAW44308	Aaw44308 Human ost
15	39	100.0	408	2	AAW89685	Aaw89685 Osteogeni
16	39	100.0	408	2	AAY43119	Aay43119 Osteogeni
17	39	100.0	408	7	ADJ62690	Adj62690 Human ost
18	39	100.0	408	8	ADE52761	Ade52761 Human ost
19	39	100.0	408	8	ADM80499	Adm80499 Human ost
20	39	100.0	408	8	ADO03621	Ado03621 Human ost
21	39	100.0	412	8	ABO84472	Abo84472 Human can
22	39	100.0	431	2	AAR07335	Aar07335 Human Bon
23	39	100.0	431	2	AAR12106	Aar12106 Mammalian
24	39	100.0	431	2	AAR23833	Aar23833 Human ost
25	39	100.0	431	2	AAR27289	Aar27289 Human ost
26	39	100.0	431	2	AAR44746	Aar44746 Osteogeni
27	39	100.0	431	2	AAR33408	Aar33408 Human OP-
28	39	100.0	431	2	AAR36734	Aar36734 Human BMP
29	39	100.0	431	2	AAR54935	Aar54935 Osteogeni
30	39	100.0	431	2	AAR46731	Aar46731 Human ost
31	39	100.0	431	2	AAR50198	Aar50198 Human OP-
32	39	100.0	431	2	AAR51644	Aar51644 hOP1 huma
33	39	100.0	431	2	AAR60577	Aar60577 Osteogeni
34	39	100.0	431	2	AAR47290	Aar47290 hOP1. 3/2
35	39	100.0	431	2	AAR50236	Aar50236 Human OP-
36	39	100.0	431	2	AAR57971	Aar57971 Human OP-
37	39	100.0	431	2	AAR47250	Aar47250 hOP1. 3/2
38	39	100.0	431	2	AAR85211	Aar85211 Human ost
39	39	100.0	431	2	AAW00236	Aaw00236 Human ost
40	39	100.0	431	2	AAR87537	Aar87537 Human ost
41	39	100.0	431	2	AAR85757	Aar85757 hOP-1. 3/
42	39	100.0	431	2	AAW16365	Aaw16365 Human hip
43	39	100.0	431	2	AAW40190	Aaw40190 Human OP-
44	39	100.0	431	2	AAW36853	Aaw36853 Full leng
45	39	100.0	431	2	AAW27508	Aaw27508 Human ost

ALIGNMENTS

RESULT 1

AAR44750

ID AAR44750 standard; protein; 317 AA.

XX

AC AAR44750;

XX

DT 25-MAR-2003 (revised)

DT 01-JUL-2002 (revised)

DT 06-JUN-1994 (first entry)

XX

DE Osteogenic fusion protein OP1B.

XX

KW Osteogenic protein; bone; cartilage; matrix; osteoarthritis; repair;

KW vascularisation; mineralisation; differentiation.

XX

Search completed: January 5, 2006, 17:24:57
Job time : 20.9947 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 5, 2006, 17:16:35 ; Search time 4.98837 Seconds
(without alignments)
646.373 Million cell updates/sec

Title: US-10-734-472-2_COPY_292_330
Perfect score: 39
Sequence: 1 RSTGSKQRSQNRSKTPKNQEALRMANVAENSSSDQRQAC 39

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result							
No.	Score	% Query Match	Length	DB	ID	Description	
1	39	100.0	317	1	US-07-841-646-11	Sequence 11, Appl	
2	39	100.0	317	1	US-08-147-023-11	Sequence 11, Appl	
3	39	100.0	317	1	US-08-447-570-11	Sequence 11, Appl	
4	39	100.0	317	1	US-08-449-700-11	Sequence 11, Appl	
5	39	100.0	317	1	US-08-449-699A-11	Sequence 11, Appl	
6	39	100.0	317	2	US-09-148-925C-11	Sequence 11, Appl	
7	39	100.0	317	2	US-08-957-425-11	Sequence 11, Appl	
8	39	100.0	317	2	US-10-321-799-11	Sequence 11, Appl	

9	39	100.0	400	1	US-07-764-731B-10	Sequence 10, Appl
10	39	100.0	408	1	US-07-841-646-15	Sequence 15, Appl
11	39	100.0	408	1	US-08-147-023-15	Sequence 15, Appl
12	39	100.0	408	1	US-08-447-570-15	Sequence 15, Appl
13	39	100.0	408	1	US-08-449-700-15	Sequence 15, Appl
14	39	100.0	408	1	US-08-449-699A-15	Sequence 15, Appl
15	39	100.0	408	2	US-09-148-925C-15	Sequence 15, Appl
16	39	100.0	408	2	US-08-957-425-15	Sequence 15, Appl
17	39	100.0	408	2	US-10-321-799-15	Sequence 15, Appl
18	39	100.0	431	1	US-07-841-646-2	Sequence 2, Appli
19	39	100.0	431	1	US-07-901-703-2	Sequence 2, Appli
20	39	100.0	431	1	US-07-539-756-4	Sequence 4, Appli
21	39	100.0	431	1	US-08-147-023-2	Sequence 2, Appli
22	39	100.0	431	1	US-08-206-864-2	Sequence 2, Appli
23	39	100.0	431	1	US-08-278-729A-17	Sequence 17, Appl
24	39	100.0	431	1	US-08-480-528A-4	Sequence 4, Appli
25	39	100.0	431	1	US-08-479-666-4	Sequence 4, Appli
26	39	100.0	431	1	US-08-155-343A-17	Sequence 17, Appl
27	39	100.0	431	1	US-08-406-672-17	Sequence 17, Appl
28	39	100.0	431	1	US-08-643-563A-17	Sequence 17, Appl
29	39	100.0	431	1	US-08-447-570-2	Sequence 2, Appli
30	39	100.0	431	1	US-08-643-763A-17	Sequence 17, Appl
31	39	100.0	431	1	US-08-462-623-17	Sequence 17, Appl
32	39	100.0	431	1	US-08-451-953A-17	Sequence 17, Appl
33	39	100.0	431	1	US-08-459-346-2	Sequence 2, Appli
34	39	100.0	431	1	US-08-445-468A-17	Sequence 17, Appl
35	39	100.0	431	1	US-08-901-200A-4	Sequence 4, Appli
36	39	100.0	431	1	US-08-481-337A-10	Sequence 10, Appl
37	39	100.0	431	1	US-08-449-700-2	Sequence 2, Appli
38	39	100.0	431	1	US-07-989-847-6	Sequence 6, Appli
39	39	100.0	431	1	US-08-449-699A-2	Sequence 2, Appli
40	39	100.0	431	1	US-08-696-268B-4	Sequence 4, Appli
41	39	100.0	431	1	US-08-461-397A-17	Sequence 17, Appl
42	39	100.0	431	1	US-08-912-088-17	Sequence 17, Appl
43	39	100.0	431	2	US-08-278-730A-17	Sequence 17, Appl
44	39	100.0	431	2	US-08-458-811-2	Sequence 2, Appli
45	39	100.0	431	2	US-08-889-419-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-07-841-646-11

; Sequence 11, Application US/07841646

; Patent No. 5266683

; GENERAL INFORMATION:

; APPLICANT: OPPERMAN, HERMANN

; APPLICANT: OZKAYNAK, ENGIN

; APPLICANT: KUBERASAMPATH, THANGAVEL

; APPLICANT: RUEGER, DAVID C.

; APPLICANT: PANG, ROY H.L.

; TITLE OF INVENTION: OSTEOGENIC DEVICES

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TESTA, HURWITZ & THIBEAULT

; STREET: 53 STATE STREET

Search completed: January 5, 2006, 17:36:57
Job time : 5.98837 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:16:50 ; Search time 16.2844 Seconds
(without alignments)
1000.675 Million cell updates/sec

Title: US-10-734-472-2_COPY_292_330
Perfect score: 39
Sequence: 1 RSTGSKQRSQNRSKTPKNQEALRMANVAENSSSDQRQAC 39

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	39	100.0	317	2	US-08-957-425-11	Sequence 11, Appl	
2	39	100.0	317	4	US-10-321-799-11	Sequence 11, Appl	
3	39	100.0	317	4	US-10-428-997A-11	Sequence 11, Appl	
4	39	100.0	408	2	US-08-957-425-15	Sequence 15, Appl	
5	39	100.0	408	4	US-10-321-799-15	Sequence 15, Appl	
6	39	100.0	408	4	US-10-428-997A-15	Sequence 15, Appl	
7	39	100.0	408	4	US-10-367-094-173	Sequence 173, App	
8	39	100.0	427	4	US-10-367-094-171	Sequence 171, App	

9	39	100.0	427	4	US-10-367-094-175	Sequence 175, App
10	39	100.0	431	2	US-08-822-186-2	Sequence 2, Appli
11	39	100.0	431	2	US-08-937-755-2	Sequence 2, Appli
12	39	100.0	431	2	US-08-957-425-2	Sequence 2, Appli
13	39	100.0	431	2	US-08-260-675-17	Sequence 17, Appl
14	39	100.0	431	3	US-09-045-331-2	Sequence 2, Appli
15	39	100.0	431	3	US-09-828-607-2	Sequence 2, Appli
16	39	100.0	431	3	US-09-887-901-2	Sequence 2, Appli
17	39	100.0	431	3	US-09-982-543A-10	Sequence 10, Appl
18	39	100.0	431	3	US-09-039-107-2	Sequence 2, Appli
19	39	100.0	431	3	US-09-798-518-1	Sequence 1, Appli
20	39	100.0	431	3	US-09-540-466-2	Sequence 2, Appli
21	39	100.0	431	3	US-09-423-943-2	Sequence 2, Appli
22	39	100.0	431	3	US-09-012-846-2	Sequence 2, Appli
23	39	100.0	431	3	US-09-960-789-1	Sequence 1, Appli
24	39	100.0	431	3	US-09-952-318A-17	Sequence 17, Appl
25	39	100.0	431	4	US-10-062-370-5	Sequence 5, Appli
26	39	100.0	431	4	US-10-083-825-2	Sequence 2, Appli
27	39	100.0	431	4	US-10-122-026-2	Sequence 2, Appli
28	39	100.0	431	4	US-10-272-503-2	Sequence 2, Appli
29	39	100.0	431	4	US-10-050-050-17	Sequence 17, Appl
30	39	100.0	431	4	US-10-286-152A-8	Sequence 8, Appli
31	39	100.0	431	4	US-10-301-822-10	Sequence 10, Appl
32	39	100.0	431	4	US-10-366-345-39	Sequence 39, Appl
33	39	100.0	431	4	US-10-321-799-2	Sequence 2, Appli
34	39	100.0	431	4	US-10-295-027-518	Sequence 518, App
35	39	100.0	431	4	US-10-295-027-787	Sequence 787, App
36	39	100.0	431	4	US-10-295-027-806	Sequence 806, App
37	39	100.0	431	4	US-10-295-027-843	Sequence 843, App
38	39	100.0	431	4	US-10-375-150-6	Sequence 6, Appli
39	39	100.0	431	4	US-10-173-999-58	Sequence 58, Appl
40	39	100.0	431	4	US-10-428-275-6	Sequence 6, Appli
41	39	100.0	431	4	US-10-428-997A-2	Sequence 2, Appli
42	39	100.0	431	4	US-10-302-812-28	Sequence 28, Appl
43	39	100.0	431	4	US-10-290-554-1	Sequence 1, Appli
44	39	100.0	431	4	US-10-753-916-2	Sequence 2, Appli
45	39	100.0	431	5	US-10-806-852-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-957-425-11

; Sequence 11, Application US/08957425

; Publication No. US20030069401A1

; GENERAL INFORMATION:

; APPLICANT: OPPERMAN, HERMANN

; OZKAYNAK, ENGIN

; KUBERASAMPATH, THANGAVEL

; RUEGER, DAVID C.

; PANG, ROY H.L.

; TITLE OF INVENTION: OSTEOGENIC DEVICES

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TESTA, HURWITZ & THIBEAULT

; STREET: 53 STATE STREET

Search completed: January 5, 2006, 17:43:38
Job time : 17.2844 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:25:10 ; Search time 0.906977 Seconds
(without alignments)
364.935 Million cell updates/sec

Title: US-10-734-472-2_COPY_292_330
Perfect score: 39
Sequence: 1 RSTGSKQRSQNRSKTPKNQEALRMANVAENSSSDQRQAC 39

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 61072 seqs, 8486849 residues

Word size : 0

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA_New:*

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- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description	
1	39	100.0	317	7	US-11-051-568-11	Sequence 11, Appl
2	39	100.0	408	7	US-11-051-568-15	Sequence 15, Appl
3	39	100.0	431	6	US-10-816-768-39	Sequence 39, Appl
4	39	100.0	431	6	US-10-650-326B-3	Sequence 3, Appli
5	39	100.0	431	7	US-11-051-568-2	Sequence 2, Appli
6	39	100.0	431	7	US-11-186-284-10	Sequence 10, Appl

7	39	100.0	484	7	US-11-051-568-13	Sequence 13, Appl
8	38	97.4	139	6	US-10-816-768-68	Sequence 68, Appl
9	38	97.4	139	6	US-10-650-326B-1	Sequence 1, Appli
10	35	89.7	46	6	US-10-816-768-91	Sequence 91, Appl
11	35	89.7	111	6	US-10-816-768-96	Sequence 96, Appl
12	24	61.5	43	6	US-10-816-768-104	Sequence 104, App
13	24	61.5	56	6	US-10-816-768-106	Sequence 106, App
14	22	56.4	64	6	US-10-816-768-108	Sequence 108, App
15	20	51.3	139	6	US-10-650-326B-4	Sequence 4, Appli
16	20	51.3	430	6	US-10-650-326B-19	Sequence 19, Appl
17	20	51.3	430	7	US-11-051-568-25	Sequence 25, Appl
18	16	41.0	117	6	US-10-816-768-69	Sequence 69, Appl
19	15	38.5	15	6	US-10-816-768-102	Sequence 102, App
20	15	38.5	80	6	US-10-816-768-94	Sequence 94, Appl
21	15	38.5	89	6	US-10-816-768-98	Sequence 98, Appl
22	9	23.1	129	6	US-10-816-768-89	Sequence 89, Appl
23	6	15.4	7	6	US-10-816-768-37	Sequence 37, Appl
24	6	15.4	482	6	US-10-055-877-298	Sequence 298, App
25	6	15.4	895	6	US-10-485-517-129	Sequence 129, App
26	6	15.4	963	6	US-10-467-962B-2	Sequence 2, Appli
27	5	12.8	7	7	US-11-096-706-91	Sequence 91, Appl
28	5	12.8	15	7	US-11-126-841A-8	Sequence 8, Appli
29	5	12.8	50	7	US-11-119-249-11	Sequence 11, Appl
30	5	12.8	54	6	US-10-467-657-7474	Sequence 7474, Ap
31	5	12.8	70	7	US-11-057-047-3	Sequence 3, Appli
32	5	12.8	96	7	US-11-212-443-162	Sequence 162, App
33	5	12.8	98	7	US-11-053-076-175	Sequence 175, App
34	5	12.8	99	6	US-10-485-788A-793	Sequence 793, App
35	5	12.8	107	6	US-10-467-657-6644	Sequence 6644, Ap
36	5	12.8	114	6	US-10-793-626-492	Sequence 492, App
37	5	12.8	122	6	US-10-821-234-1239	Sequence 1239, Ap
38	5	12.8	140	6	US-10-793-626-1806	Sequence 1806, Ap
39	5	12.8	142	6	US-10-995-561-680	Sequence 680, App
40	5	12.8	144	6	US-10-467-657-2342	Sequence 2342, Ap
41	5	12.8	169	7	US-11-051-568-9	Sequence 9, Appli
42	5	12.8	177	7	US-11-076-164-4	Sequence 4, Appli
43	5	12.8	185	6	US-10-467-657-144	Sequence 144, App
44	5	12.8	185	6	US-10-467-657-4092	Sequence 4092, Ap
45	5	12.8	185	6	US-10-467-657-7068	Sequence 7068, Ap

ALIGNMENTS

RESULT 1

US-11-051-568-11

; Sequence 11, Application US/11051568

; Publication No. US20050255141A1

; GENERAL INFORMATION:

; APPLICANT: OPPERMAN, HERMANN

; OZKAYNAK, ENGIN

; KUBERASAMPATH, THANGAVEL

; RUEGER, DAVID C.

; PANG, ROY H.L.

; TITLE OF INVENTION: OSTEOGENIC DEVICES

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

OM protein - protein search, using sw model

Run on: January 5, 2006, 17:13:39 ; Search time 3.38055 Seconds
(without alignments)
1110.013 Million cell updates/sec

Title: US-10-734-472-2_COPY_292_330
Perfect score: 39
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	39	100.0	431	1	BMHU7	bone morphogenetic
2	20	51.3	430	2	JQ1184	osteogenic protein
3	16	41.0	313	2	I51284	bone morphogenetic
4	7	17.9	398	2	T34233	hypothetical prote
5	7	17.9	402	2	F96640	hypothetical prote
6	6	15.4	125	2	C70637	hypothetical prote
7	6	15.4	130	2	H65019	hypothetical prote
8	6	15.4	150	2	F87507	conserved hypothet
9	6	15.4	160	2	E71560	hypothetical prote
10	6	15.4	161	2	C81711	conserved hypothet
11	6	15.4	179	2	B71274	probable translati
12	6	15.4	181	2	B83699	methylphosphotries
13	6	15.4	199	2	JH0822	lymphocyte early a

14	6	15.4	207	1	A35685	metalloproteinase
15	6	15.4	207	2	I47061	collagenase inhibi
16	6	15.4	207	2	I46964	metalloproteinase
17	6	15.4	212	2	B75156	resolvase related
18	6	15.4	220	2	T21730	hypothetical prote
19	6	15.4	240	2	A96680	hypothetical prote
20	6	15.4	253	2	F69181	transcription regu
21	6	15.4	254	2	T07387	14-3-3 protein tft
22	6	15.4	258	2	T07389	14-3-3 protein tft
23	6	15.4	290	2	A82236	pseudouridine synt
24	6	15.4	290	2	T05009	hypothetical prote
25	6	15.4	301	2	T16844	hypothetical prote
26	6	15.4	304	2	T48281	hypothetical prote
27	6	15.4	311	2	E95865	probable CbbX prot
28	6	15.4	318	2	B48487	MocB (Tn4399) - Ba
29	6	15.4	321	2	E81301	hypothetical prote
30	6	15.4	325	2	H84230	transcription init
31	6	15.4	326	2	A83273	fatty acid biosynt
32	6	15.4	331	2	E71854	hypothetical prote
33	6	15.4	334	2	A38214	meiosis-specific r
34	6	15.4	335	2	A60328	40K cell wall prot
35	6	15.4	339	1	C43684	capsid protein 37K
36	6	15.4	340	2	JN0527	tcpE protein precu
37	6	15.4	340	2	JN0525	toxin co-regulated
38	6	15.4	346	2	H90849	hypothetical prote
39	6	15.4	346	2	G85707	unknown protein en
40	6	15.4	364	2	T05989	hypothetical prote
41	6	15.4	366	2	S46736	hypothetical prote
42	6	15.4	370	2	AB0602	probable membrane
43	6	15.4	372	2	B64819	probable membrane
44	6	15.4	372	2	B85591	hypothetical prote
45	6	15.4	372	2	G90740	hypothetical prote

ALIGNMENTS

RESULT 1

BMHU7

bone morphogenetic protein 7 precursor - human

N;Alternate names: osteogenic protein 1

C;Species: Homo sapiens (man)

C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: C39263; S10529

R;Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozney, J.M.

Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990

A;Title: Identification of transforming growth factor beta family members present in bone-inductive protein purified from bovine bone.

A;Reference number: A39263; MUID:91088608; PMID:2263636

A;Accession: C39263

A;Molecule type: mRNA

A;Residues: 1-431 <CEL>

A;Cross-references: UNIPROT:P18075; UNIPARC:UPI00000349AD; GB:M60316; GB:M38695;

NID:g339563; PIDN:AAA36738.1; PID:g339564

R;Oezkaynak, E.; Rueger, D.C.; Drier, E.A.; Corbett, C.; Ridge, R.J.; Sampath, T.K.; Oppermann, H.

A;Accession: I47061
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-207 <TAN>
A;Cross-references: UNIPROT:P35624; UNIPARC:UPI000016C64A; GB:S96211;
NID:g247729; PIDN:AAB21865.1; PID:g247730
C;Superfamily: metalloproteinase inhibitor

Query Match 15.4%; Score 6; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RSQNRS 13
 |||||
Db 98 RSQNRS 103

Search completed: January 5, 2006, 17:34:51
Job time : 4.38055 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:12:49 ; Search time 20.6131 Seconds
(without alignments)
1334.860 Million cell updates/sec

Title: US-10-734-472-2_COPY_292_330
Perfect score: 39
Sequence: 1 RSTGSKQRSQNRSKTPKNQEALRMANVAENSSSDQRQAC 39

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	39	100.0	412	2		Q9BTB3_HUMAN	Q9btb3 homo sapien
2	39	100.0	431	1		BMP7_HUMAN	P18075 homo sapien
3	20	51.3	141	2		O88684_RAT	O88684 rattus norv
4	20	51.3	306	2		Q9R228_RAT	Q9r228 rattus norv
5	20	51.3	430	1		BMP7_MOUSE	P23359 mus musculu
6	18	46.2	365	2		Q5U916_PIG	Q5u916 sus scrofa
7	16	41.0	313	2		Q91403_CHICK	Q91403 gallus gall
8	16	41.0	398	2		Q9I8T6_CHICK	Q9i8t6 gallus gall
9	15	38.5	108	2		Q8MJCO_SHEEP	Q8mjc0 ovis aries
10	15	38.5	206	2		Q95L63_RABIT	Q95l63 oryctolagus
11	8	20.5	672	2		Q7QEL1_ANOGA	Q7qell anopheles g
12	7	17.9	281	2		Q7PS23_ANOGA	Q7ps23 anopheles g

OM protein - protein search, using sw model

Run on: January 5, 2006, 17:12:04 ; Search time 71.7759 Seconds
(without alignments)
857.015 Million cell updates/sec

Title: US-10-734-472-2_COPY_292_431
Perfect score: 140
Sequence: 1 RSTGSKQRSQNRSKTPKNQE.....SSNVILKKYRNMVVRACGCH 140

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	140	100.0	317	2	AAR51656	Aar51656 Osteogeni
2	140	100.0	317	2	AAR85766	Aar85766 OP1B fusi
3	140	100.0	317	2	AAW44306	Aaw44306 Human ost
4	140	100.0	317	2	AAW89683	Aaw89683 Osteogeni
5	140	100.0	317	2	AAY43117	Aay43117 Osteogeni
6	140	100.0	317	7	ADJ62686	Adj62686 Human ost
7	140	100.0	317	8	ADE52757	Ade52757 Human ost
8	140	100.0	317	8	ADM80495	Adm80495 Human ost

9	140	100.0	317	8	ADO03617	Ado03617	Human ost
10	140	100.0	408	2	AAR44752	Aar44752	Osteogeni
11	140	100.0	408	2	AAR51658	Aar51658	Osteogeni
12	140	100.0	408	2	AAR85768	Aar85768	OP1D fusi
13	140	100.0	408	2	AAW44308	Aaw44308	Human ost
14	140	100.0	408	2	AAW89685	Aaw89685	Osteogeni
15	140	100.0	408	2	AAY43119	Aay43119	Osteogeni
16	140	100.0	408	7	ADJ62690	Adj62690	Human ost
17	140	100.0	408	8	ADE52761	Ade52761	Human ost
18	140	100.0	408	8	ADM80499	Adm80499	Human ost
19	140	100.0	408	8	ADO03621	Ado03621	Human ost
20	140	100.0	431	2	AAR07335	Aar07335	Human Bon
21	140	100.0	431	2	AAR12106	Aar12106	Mammalian
22	140	100.0	431	2	AAR23833	Aar23833	Human ost
23	140	100.0	431	2	AAR27289	Aar27289	Human ost
24	140	100.0	431	2	AAR44746	Aar44746	Osteogeni
25	140	100.0	431	2	AAR33408	Aar33408	Human OP-
26	140	100.0	431	2	AAR36734	Aar36734	Human BMP
27	140	100.0	431	2	AAR54935	Aar54935	Osteogeni
28	140	100.0	431	2	AAR46731	Aar46731	Human ost
29	140	100.0	431	2	AAR50198	Aar50198	Human OP-
30	140	100.0	431	2	AAR51644	Aar51644	hOP1 huma
31	140	100.0	431	2	AAR60577	Aar60577	Osteogeni
32	140	100.0	431	2	AAR47290	Aar47290	hOP1. 3/2
33	140	100.0	431	2	AAR50236	Aar50236	Human OP-
34	140	100.0	431	2	AAR57971	Aar57971	Human OP-
35	140	100.0	431	2	AAR47250	Aar47250	hOP1. 3/2
36	140	100.0	431	2	AAR85211	Aar85211	Human ost
37	140	100.0	431	2	AAW00236	Aaw00236	Human ost
38	140	100.0	431	2	AAR87537	Aar87537	Human ost
39	140	100.0	431	2	AAR85757	Aar85757	hOP-1. 3/
40	140	100.0	431	2	AAW16365	Aaw16365	Human hip
41	140	100.0	431	2	AAW40190	Aaw40190	Human OP-
42	140	100.0	431	2	AAW36853	Aaw36853	Full leng
43	140	100.0	431	2	AAW27508	Aaw27508	Human ost
44	140	100.0	431	2	AAW34783	Aaw34783	Human ost
45	140	100.0	431	2	AAW53179	Aaw53179	Human ost

ALIGNMENTS

RESULT 1

AAR51656

ID AAR51656 standard; protein; 317 AA.

XX

AC AAR51656;

XX

DT 25-MAR-2003 (revised)

DT 01-JUL-2002 (revised)

DT 09-JUN-1995 (first entry)

XX

DE Osteogenic fusion protein 1B OP1B.

XX

KW Osteogenic protein 1A; OP1B; osteoarthritis; osteogenesis;

KW cartilage and endochondrial bone formation; allograft repair;

KW periodontal, dental and craniofacial reconstruction;

Search completed: January 5, 2006, 17:24:57
Job time : 71.7759 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:16:35 ; Search time 17.907 Seconds
(without alignments)
646.373 Million cell updates/sec

Title: US-10-734-472-2_COPY_292_431
Perfect score: 140
Sequence: 1 RSTGSKQRSQNRSKTPKNQE.....SSNVILKKYRNMVVRACGCH 140

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	140	100.0	317	1	US-07-841-646-11 Sequence 11, Appl
2	140	100.0	317	1	US-08-147-023-11 Sequence 11, Appl
3	140	100.0	317	1	US-08-447-570-11 Sequence 11, Appl
4	140	100.0	317	1	US-08-449-700-11 Sequence 11, Appl
5	140	100.0	317	1	US-08-449-699A-11 Sequence 11, Appl
6	140	100.0	317	2	US-09-148-925C-11 Sequence 11, Appl
7	140	100.0	317	2	US-08-957-425-11 Sequence 11, Appl
8	140	100.0	317	2	US-10-321-799-11 Sequence 11, Appl

9	140	100.0	400	1	US-07-764-731B-10	Sequence 10, Appl
10	140	100.0	408	1	US-07-841-646-15	Sequence 15, Appl
11	140	100.0	408	1	US-08-147-023-15	Sequence 15, Appl
12	140	100.0	408	1	US-08-447-570-15	Sequence 15, Appl
13	140	100.0	408	1	US-08-449-700-15	Sequence 15, Appl
14	140	100.0	408	1	US-08-449-699A-15	Sequence 15, Appl
15	140	100.0	408	2	US-09-148-925C-15	Sequence 15, Appl
16	140	100.0	408	2	US-08-957-425-15	Sequence 15, Appl
17	140	100.0	408	2	US-10-321-799-15	Sequence 15, Appl
18	140	100.0	431	1	US-07-841-646-2	Sequence 2, Appli
19	140	100.0	431	1	US-07-901-703-2	Sequence 2, Appli
20	140	100.0	431	1	US-07-539-756-4	Sequence 4, Appli
21	140	100.0	431	1	US-08-147-023-2	Sequence 2, Appli
22	140	100.0	431	1	US-08-206-864-2	Sequence 2, Appli
23	140	100.0	431	1	US-08-278-729A-17	Sequence 17, Appl
24	140	100.0	431	1	US-08-480-528A-4	Sequence 4, Appli
25	140	100.0	431	1	US-08-479-666-4	Sequence 4, Appli
26	140	100.0	431	1	US-08-155-343A-17	Sequence 17, Appl
27	140	100.0	431	1	US-08-406-672-17	Sequence 17, Appl
28	140	100.0	431	1	US-08-643-563A-17	Sequence 17, Appl
29	140	100.0	431	1	US-08-447-570-2	Sequence 2, Appli
30	140	100.0	431	1	US-08-643-763A-17	Sequence 17, Appl
31	140	100.0	431	1	US-08-462-623-17	Sequence 17, Appl
32	140	100.0	431	1	US-08-451-953A-17	Sequence 17, Appl
33	140	100.0	431	1	US-08-459-346-2	Sequence 2, Appli
34	140	100.0	431	1	US-08-445-468A-17	Sequence 17, Appl
35	140	100.0	431	1	US-08-901-200A-4	Sequence 4, Appli
36	140	100.0	431	1	US-08-481-337A-10	Sequence 10, Appl
37	140	100.0	431	1	US-08-449-700-2	Sequence 2, Appli
38	140	100.0	431	1	US-07-989-847-6	Sequence 6, Appli
39	140	100.0	431	1	US-08-449-699A-2	Sequence 2, Appli
40	140	100.0	431	1	US-08-696-268B-4	Sequence 4, Appli
41	140	100.0	431	1	US-08-461-397A-17	Sequence 17, Appl
42	140	100.0	431	1	US-08-912-088-17	Sequence 17, Appl
43	140	100.0	431	2	US-08-278-730A-17	Sequence 17, Appl
44	140	100.0	431	2	US-08-458-811-2	Sequence 2, Appli
45	140	100.0	431	2	US-08-889-419-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-07-841-646-11
; Sequence 11, Application US/07841646
; Patent No. 5266683
; GENERAL INFORMATION:
;   APPLICANT:  OPPERMANN, HERMANN
;   APPLICANT:  OZKAYNAK, ENGIN
;   APPLICANT:  KUBERASAMPATH, THANGAVEL
;   APPLICANT:  RUEGER, DAVID C.
;   APPLICANT:  PANG, ROY H.L.
;   TITLE OF INVENTION:  OSTEOGENIC DEVICES
;   NUMBER OF SEQUENCES:  33
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  TESTA, HURWITZ & THIBEAULT
;     STREET:    53 STATE STREET

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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:16:50 ; Search time 58.4567 Seconds
(without alignments)
1000.675 Million cell updates/sec

Title: US-10-734-472-2_COPY_292_431
Perfect score: 140
Sequence: 1 RSTGSKQRSQNRSKTPKNQE.....SSNVILKKYRNMVVRACGCH 140

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	140	100.0	317	2	US-08-957-425-11	Sequence 11, Appl
2	140	100.0	317	4	US-10-321-799-11	Sequence 11, Appl
3	140	100.0	317	4	US-10-428-997A-11	Sequence 11, Appl
4	140	100.0	408	2	US-08-957-425-15	Sequence 15, Appl
5	140	100.0	408	4	US-10-321-799-15	Sequence 15, Appl
6	140	100.0	408	4	US-10-428-997A-15	Sequence 15, Appl
7	140	100.0	427	4	US-10-367-094-171	Sequence 171, App
8	140	100.0	427	4	US-10-367-094-175	Sequence 175, App
9	140	100.0	431	2	US-08-822-186-2	Sequence 2, Appli
10	140	100.0	431	2	US-08-937-755-2	Sequence 2, Appli
11	140	100.0	431	2	US-08-957-425-2	Sequence 2, Appli
12	140	100.0	431	2	US-08-260-675-17	Sequence 17, Appl
13	140	100.0	431	3	US-09-045-331-2	Sequence 2, Appli
14	140	100.0	431	3	US-09-828-607-2	Sequence 2, Appli
15	140	100.0	431	3	US-09-887-901-2	Sequence 2, Appli

16	140	100.0	431	3	US-09-982-543A-10	Sequence 10, Appl
17	140	100.0	431	3	US-09-039-107-2	Sequence 2, Appli
18	140	100.0	431	3	US-09-798-518-1	Sequence 1, Appli
19	140	100.0	431	3	US-09-540-466-2	Sequence 2, Appli
20	140	100.0	431	3	US-09-423-943-2	Sequence 2, Appli
21	140	100.0	431	3	US-09-012-846-2	Sequence 2, Appli
22	140	100.0	431	3	US-09-960-789-1	Sequence 1, Appli
23	140	100.0	431	3	US-09-952-318A-17	Sequence 17, Appl
24	140	100.0	431	4	US-10-062-370-5	Sequence 5, Appli
25	140	100.0	431	4	US-10-083-825-2	Sequence 2, Appli
26	140	100.0	431	4	US-10-122-026-2	Sequence 2, Appli
27	140	100.0	431	4	US-10-272-503-2	Sequence 2, Appli
28	140	100.0	431	4	US-10-050-050-17	Sequence 17, Appl
29	140	100.0	431	4	US-10-286-152A-8	Sequence 8, Appli
30	140	100.0	431	4	US-10-301-822-10	Sequence 10, Appl
31	140	100.0	431	4	US-10-366-345-39	Sequence 39, Appl
32	140	100.0	431	4	US-10-321-799-2	Sequence 2, Appli
33	140	100.0	431	4	US-10-295-027-518	Sequence 518, App
34	140	100.0	431	4	US-10-295-027-787	Sequence 787, App
35	140	100.0	431	4	US-10-295-027-806	Sequence 806, App
36	140	100.0	431	4	US-10-295-027-843	Sequence 843, App
37	140	100.0	431	4	US-10-375-150-6	Sequence 6, Appli
38	140	100.0	431	4	US-10-173-999-58	Sequence 58, Appl
39	140	100.0	431	4	US-10-428-275-6	Sequence 6, Appli
40	140	100.0	431	4	US-10-428-997A-2	Sequence 2, Appli
41	140	100.0	431	4	US-10-302-812-28	Sequence 28, Appl
42	140	100.0	431	4	US-10-290-554-1	Sequence 1, Appli
43	140	100.0	431	4	US-10-753-916-2	Sequence 2, Appli
44	140	100.0	431	5	US-10-806-852-2	Sequence 2, Appli
45	140	100.0	431	5	US-10-995-979-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-957-425-11

; Sequence 11, Application US/08957425

; Publication No. US20030069401A1

; GENERAL INFORMATION:

; APPLICANT: OPFERMANN, HERMANN

; OZKAYNAK, ENGIN

; KUBERASAMPATH, THANGAVEL

; RUEGER, DAVID C.

; PANG, ROY H.L.

; TITLE OF INVENTION: OSTEOGENIC DEVICES

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TESTA, HURWITZ & THIBEAULT

; STREET: 53 STATE STREET

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: U.S.A.

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

Search completed: January 5, 2006, 17:43:38
Job time : 58.4567 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:25:10 ; Search time 3.25581 Seconds
(without alignments)
364.935 Million cell updates/sec

Title: US-10-734-472-2_COPY_292_431
Perfect score: 140
Sequence: 1 RSTGSKQRSQNRSKTPKNQE.....SSNVILKKYRNMVVVRACGCH 140

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 61072 seqs, 8486849 residues

Word size : 0

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	140	100.0	317	7	US-11-051-568-11	Sequence 11, Appl
2	140	100.0	408	7	US-11-051-568-15	Sequence 15, Appl
3	140	100.0	431	6	US-10-816-768-39	Sequence 39, Appl
4	140	100.0	431	6	US-10-650-326B-3	Sequence 3, Appli
5	140	100.0	431	7	US-11-051-568-2	Sequence 2, Appli
6	140	100.0	431	7	US-11-186-284-10	Sequence 10, Appl

7	140	100.0	484	7	US-11-051-568-13	Sequence 13, Appl
8	139	99.3	139	6	US-10-650-326B-1	Sequence 1, Appli
9	128	91.4	139	6	US-10-816-768-68	Sequence 68, Appl
10	106	75.7	117	6	US-10-816-768-69	Sequence 69, Appl
11	106	75.7	169	7	US-11-051-568-9	Sequence 9, Appli
12	102	72.9	102	6	US-10-816-768-55	Sequence 55, Appl
13	80	57.1	129	6	US-10-816-768-89	Sequence 89, Appl
14	71	50.7	139	6	US-10-650-326B-4	Sequence 4, Appli
15	71	50.7	430	6	US-10-650-326B-19	Sequence 19, Appl
16	71	50.7	430	7	US-11-051-568-25	Sequence 25, Appl
17	38	27.1	39	6	US-10-816-768-112	Sequence 112, App
18	35	25.0	46	6	US-10-816-768-91	Sequence 91, Appl
19	35	25.0	111	6	US-10-816-768-96	Sequence 96, Appl
20	30	21.4	39	6	US-10-816-768-121	Sequence 121, App
21	29	20.7	454	6	US-10-650-326B-15	Sequence 15, Appl
22	28	20.0	39	6	US-10-816-768-113	Sequence 113, App
23	28	20.0	39	6	US-10-816-768-114	Sequence 114, App
24	28	20.0	39	6	US-10-816-768-122	Sequence 122, App
25	28	20.0	39	6	US-10-816-768-123	Sequence 123, App
26	27	19.3	102	6	US-10-816-768-52	Sequence 52, Appl
27	26	18.6	35	6	US-10-816-768-5	Sequence 5, Appli
28	24	17.1	39	6	US-10-816-768-110	Sequence 110, App
29	24	17.1	43	6	US-10-816-768-104	Sequence 104, App
30	24	17.1	56	6	US-10-816-768-106	Sequence 106, App
31	22	15.7	64	6	US-10-816-768-108	Sequence 108, App
32	20	14.3	39	6	US-10-816-768-118	Sequence 118, App
33	19	13.6	35	6	US-10-816-768-6	Sequence 6, Appli
34	19	13.6	102	6	US-10-816-768-47	Sequence 47, Appl
35	19	13.6	438	6	US-10-650-326B-9	Sequence 9, Appli
36	19	13.6	513	6	US-10-650-326B-16	Sequence 16, Appl
37	19	13.6	513	7	US-11-000-463-816	Sequence 816, App
38	18	12.9	39	6	US-10-816-768-117	Sequence 117, App
39	18	12.9	39	6	US-10-816-768-119	Sequence 119, App
40	18	12.9	39	6	US-10-816-768-120	Sequence 120, App
41	17	12.1	39	6	US-10-816-768-115	Sequence 115, App
42	17	12.1	39	6	US-10-816-768-116	Sequence 116, App
43	15	10.7	15	6	US-10-816-768-102	Sequence 102, App
44	15	10.7	80	6	US-10-816-768-94	Sequence 94, Appl
45	15	10.7	89	6	US-10-816-768-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1

US-11-051-568-11

; Sequence 11, Application US/11051568

; Publication No. US20050255141A1

; GENERAL INFORMATION:

; APPLICANT: OPPERMAN, HERMANN

; OZKAYNAK, ENGIN

; KUBERASAMPATH, THANGAVEL

; RUEGER, DAVID C.

; PANG, ROY H.L.

; TITLE OF INVENTION: OSTEOGENIC DEVICES

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

Run on: January 5, 2006, 17:13:39 ; Search time 12.1353 Seconds
 (without alignments)
 1110.013 Million cell updates/sec

Title: US-10-734-472-2_COPY_292_431
 Perfect score: 140
 Sequence: 1 RSTGSKQRSQNRSKTPKNQE.....SSNVILKKYRNMVVRACGCH 140

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	140	100.0	431	1	BMHU7	bone morphogenetic
2	113	80.7	313	2	I51284	bone morphogenetic
3	71	50.7	430	2	JQ1184	osteogenic protein
4	32	22.9	426	2	JH0690	bone morphogenetic
5	29	20.7	452	2	I49542	bone morphogenetic
6	29	20.7	454	1	BMHU5	bone morphogenetic
7	19	13.6	207	2	S37618	vgr protein - rat
8	19	13.6	510	2	A54798	Vg-1-related prote
9	19	13.6	513	1	BMHU6	bone morphogenetic
10	14	10.0	34	2	A36626	osteogenic protein
11	14	10.0	455	2	A43918	TGF-beta-related p
12	13	9.3	461	2	S52408	SPDVR1 protein - s
13	10	7.1	351	2	A34201	bone morphogenetic
14	10	7.1	353	2	I50607	bone morphogenetic
15	10	7.1	393	2	S37073	bone morphogenetic
16	10	7.1	394	2	S45355	bone morphogenetic
17	10	7.1	396	1	BMHU2	bone morphogenetic
18	10	7.1	398	2	JH0688	bone morphogenetic
19	10	7.1	398	2	JH0687	bone morphogenetic

20	10	7.1	400	2	A49147	bone morphogenetic
21	10	7.1	401	2	JH0689	bone morphogenetic
22	10	7.1	405	2	I50608	bone morphogenetic
23	10	7.1	408	1	BMHU4	bone morphogenetic
24	10	7.1	408	2	S58791	bone morphogenetic
25	10	7.1	408	2	JH0801	bone morphogenetic
26	10	7.1	408	2	S38343	bone morphogenetic
27	10	7.1	420	2	I49541	bone morphogenetic
28	9	6.4	427	2	A40735	TGF beta homolog d
29	8	5.7	402	2	A45056	osteogenic protein
30	7	5.0	124	2	AD0270	hypothetical prote
31	7	5.0	347	2	T50990	hypothetical prote
32	7	5.0	365	2	T43286	cet-1 protein - Ca
33	7	5.0	373	2	A41918	transforming growt
34	7	5.0	379	2	T29518	hypothetical prote
35	7	5.0	398	2	T34233	hypothetical prote
36	7	5.0	402	2	F96640	hypothetical prote
37	7	5.0	464	2	T50955	hypothetical prote
38	7	5.0	475	2	S49886	probable membrane
39	7	5.0	496	2	G96516	hypothetical prote
40	7	5.0	571	2	E90027	urease alpha subun
41	7	5.0	2206	1	GNNY21	genome polyprotein
42	6	4.3	33	2	B36193	inhibin beta-A cha
43	6	4.3	47	2	B36626	osteogenic protein
44	6	4.3	48	2	F64086	glycerol-3-phospha
45	6	4.3	67	2	A69342	hypothetical prote

ALIGNMENTS

RESULT 1

BMHU7

bone morphogenetic protein 7 precursor - human

N;Alternate names: osteogenic protein 1

C;Species: Homo sapiens (man)

C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: C39263; S10529

R;Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozney, J.M.

Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990

A;Title: Identification of transforming growth factor beta family members present in bone-inductive protein purified from bovine bone.

A;Reference number: A39263; MUID:91088608; PMID:2263636

A;Accession: C39263

A;Molecule type: mRNA

A;Residues: 1-431 <CEL>

A;Cross-references: UNIPROT:P18075; UNIPARC:UPI00000349AD; GB:M60316; GB:M38695; NID:g339563; PIDN:AAA36738.1; PID:g339564

R;Oezkaynak, E.; Rueger, D.C.; Drier, E.A.; Corbett, C.; Ridge, R.J.; Sampath, T.K.; Oppermann, H.

EMBO J. 9, 2085-2093, 1990

A;Title: OP-1 cDNA encodes an osteogenic protein in the TGF-beta family.

A;Reference number: S10529; MUID:90291971; PMID:2357959

A;Accession: S10529

A;Molecule type: mRNA

A;Residues: 1-431 <OEZ>

A;Cross-references: UNIPROT:Q90751; UNIPARC:UPI0000126A1F; EMBL:X75914;
NID:g472927; PIDN:CAA53513.1; PID:g472928
C;Genetics:
A;Gene: Bmp-2
C;Superfamily: inhibin

Query Match 7.1%; Score 10; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 TNHAIVQTLV 92
|||
Db 297 TNHAIVQTLV 306

RESULT 15

S37073

bone morphogenetic protein 2 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: S37073

R;Feng, J.Q.; Chen, D.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.
submitted to the EMBL Data Library, September 1993

A;Description: cDNA sequence of fetal rat calvarial osteoblast bone
morphogenetic protein 2.

A;Reference number: S37073

A;Accession: S37073

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-393 <FEN>

A;Cross-references: UNIPROT:P49001; UNIPARC:UPI0000126A23; EMBL:Z25868;

NID:g397950; PIDN:CAA81088.1; PID:g397951

C;Superfamily: inhibin

Query Match 7.1%; Score 10; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 TNHAIVQTLV 92
|||
Db 337 TNHAIVQTLV 346

Search completed: January 5, 2006, 17:34:52
Job time : 13.1353 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:12:49 ; Search time 73.9958 Seconds
(without alignments)
1334.860 Million cell updates/sec

Title: US-10-734-472-2_COPY_292_431
Perfect score: 140
Sequence: 1 RSTGSKQRSQNRSKTPKNQE.....SSNVILKKYRNMVVRACGCH 140

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	140	100.0	431	1	BMP7_HUMAN	P18075 homo sapien
2	113	80.7	313	2	Q91403_CHICK	Q91403 gallus gall
3	113	80.7	398	2	Q9I8T6_CHICK	Q9i8t6 gallus gall
4	94	67.1	108	2	Q8MJC0_SHEEP	Q8mjc0 ovis aries
5	92	65.7	412	2	Q9BTB3_HUMAN	Q9btb3 homo sapien
6	71	50.7	141	2	O88684_RAT	O88684 rattus norv
7	71	50.7	430	1	BMP7_MOUSE	P23359 mus musculu
8	60	42.9	365	2	Q5U916_PIG	Q5u916 sus scrofa
9	56	40.0	446	2	Q4S5J3_TETNG	Q4s5j3 tetraodon n
10	53	37.9	306	2	Q9R228_RAT	Q9r228 rattus norv
11	52	37.1	206	2	Q95L63_RABIT	Q95l63 oryctolagus
12	49	35.0	49	2	Q9MZL9_CANFA	Q9mzl9 canis famil

OM protein - protein search, using sw model

Run on: January 5, 2006, 17:12:04 ; Search time 206.099 Seconds
(without alignments)
857.015 Million cell updates/sec

Title: US-10-734-472-2_COPY_30_431
Perfect score: 402
Sequence: 1 DFSLDNEVHSSFIHRRRLRSQ.....SSNVILKKYRNMVVRACGCH 402

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	402	100.0	431	2 AAR07335	Aar07335 Human Bon
2	402	100.0	431	2 AAR12106	Aar12106 Mammalian
3	402	100.0	431	2 AAR27289	Aar27289 Human ost
4	402	100.0	431	2 AAR44746	Aar44746 Osteogeni
5	402	100.0	431	2 AAR33408	Aar33408 Human OP-
6	402	100.0	431	2 AAR54935	Aar54935 Osteogeni
7	402	100.0	431	2 AAR46731	Aar46731 Human ost
8	402	100.0	431	2 AAR50198	Aar50198 Human OP-

9	402	100.0	431	2	AAR51644	Aar51644	hOP1 huma
10	402	100.0	431	2	AAR60577	Aar60577	Osteogeni
11	402	100.0	431	2	AAR47290	Aar47290	hOP1. 3/2
12	402	100.0	431	2	AAR50236	Aar50236	Human OP-
13	402	100.0	431	2	AAR57971	Aar57971	Human OP-
14	402	100.0	431	2	AAR47250	Aar47250	hOP1. 3/2
15	402	100.0	431	2	AAW00236	Aaw00236	Human ost
16	402	100.0	431	2	AAR87537	Aar87537	Human ost
17	402	100.0	431	2	AAR85757	Aar85757	hOP-1. 3/
18	402	100.0	431	2	AAW16365	Aaw16365	Human hip
19	402	100.0	431	2	AAW40190	Aaw40190	Human OP-
20	402	100.0	431	2	AAW36853	Aaw36853	Full leng
21	402	100.0	431	2	AAW27508	Aaw27508	Human ost
22	402	100.0	431	2	AAW34783	Aaw34783	Human ost
23	402	100.0	431	2	AAW53179	Aaw53179	Human ost
24	402	100.0	431	2	AAW44302	Aaw44302	Human ost
25	402	100.0	431	2	AAW71356	Aaw71356	Human ost
26	402	100.0	431	2	AAW80749	Aaw80749	Human ost
27	402	100.0	431	2	AAW59764	Aaw59764	Morphogen
28	402	100.0	431	2	AAY17391	Aay17391	Human ost
29	402	100.0	431	2	AAW86382	Aaw86382	Human ost
30	402	100.0	431	2	AAY28656	Aay28656	Human ost
31	402	100.0	431	2	AAW89679	Aaw89679	Human ost
32	402	100.0	431	2	AAW95448	Aaw95448	Human ost
33	402	100.0	431	2	AAY24093	Aay24093	Human ost
34	402	100.0	431	2	AAY42797	Aay42797	Human ost
35	402	100.0	431	2	AAY43108	Aay43108	Human ost
36	402	100.0	431	2	AAW86339	Aaw86339	Human ost
37	402	100.0	431	2	AAY18144	Aay18144	Human OP-
38	402	100.0	431	3	AAY92587	Aay92587	Morphogen
39	402	100.0	431	3	AAB09518	Aab09518	Human mor
40	402	100.0	431	3	AAY92442	Aay92442	Human ost
41	402	100.0	431	3	AAY82158	Aay82158	Human ost
42	402	100.0	431	3	AAY57229	Aay57229	Human ost
43	402	100.0	431	3	AAB02784	Aab02784	Human mor
44	402	100.0	431	3	AAY97369	Aay97369	Human ost
45	402	100.0	431	3	AAB08841	Aab08841	Amino aci

ALIGNMENTS

RESULT 1

AAR07335

ID AAR07335 standard; protein; 431 AA.

XX

AC AAR07335;

XX

DT 25-MAR-2003 (revised)

DT 30-JAN-1991 (first entry)

XX

DE Human Bone Morphogenesis Protein-7.

XX

KW human bone morphogenic protein-7; wound healing; tissue repair;

KW cartilage formation.

XX

OS Homo sapiens.

OM protein - protein search, using sw model

Run on: January 5, 2006, 17:16:35 ; Search time 51.4186 Seconds
 (without alignments)
 646.373 Million cell updates/sec

Title: US-10-734-472-2_COPY_30_431
 Perfect score: 402
 Sequence: 1 DFSLDNEVHSSFIHRRQRSQ.....SSNVILKKYRNMVVRACGCH 402

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	402	100.0	431	1	US-07-841-646-2	Sequence 2, Appli
2	402	100.0	431	1	US-07-901-703-2	Sequence 2, Appli
3	402	100.0	431	1	US-07-539-756-4	Sequence 4, Appli
4	402	100.0	431	1	US-08-147-023-2	Sequence 2, Appli
5	402	100.0	431	1	US-08-206-864-2	Sequence 2, Appli
6	402	100.0	431	1	US-08-278-729A-17	Sequence 17, Appl
7	402	100.0	431	1	US-08-480-528A-4	Sequence 4, Appli
8	402	100.0	431	1	US-08-479-666-4	Sequence 4, Appli
9	402	100.0	431	1	US-08-155-343A-17	Sequence 17, Appl
10	402	100.0	431	1	US-08-406-672-17	Sequence 17, Appl
11	402	100.0	431	1	US-08-643-563A-17	Sequence 17, Appl

12	402	100.0	431	1	US-08-447-570-2	Sequence 2, Appli
13	402	100.0	431	1	US-08-643-763A-17	Sequence 17, Appl
14	402	100.0	431	1	US-08-462-623-17	Sequence 17, Appl
15	402	100.0	431	1	US-08-451-953A-17	Sequence 17, Appl
16	402	100.0	431	1	US-08-459-346-2	Sequence 2, Appli
17	402	100.0	431	1	US-08-445-468A-17	Sequence 17, Appl
18	402	100.0	431	1	US-08-901-200A-4	Sequence 4, Appli
19	402	100.0	431	1	US-08-481-337A-10	Sequence 10, Appl
20	402	100.0	431	1	US-08-449-700-2	Sequence 2, Appli
21	402	100.0	431	1	US-07-989-847-6	Sequence 6, Appli
22	402	100.0	431	1	US-08-449-699A-2	Sequence 2, Appli
23	402	100.0	431	1	US-08-696-268B-4	Sequence 4, Appli
24	402	100.0	431	1	US-08-461-397A-17	Sequence 17, Appl
25	402	100.0	431	1	US-08-912-088-17	Sequence 17, Appl
26	402	100.0	431	2	US-08-278-730A-17	Sequence 17, Appl
27	402	100.0	431	2	US-08-458-811-2	Sequence 2, Appli
28	402	100.0	431	2	US-08-889-419-2	Sequence 2, Appli
29	402	100.0	431	2	US-08-445-467-17	Sequence 17, Appl
30	402	100.0	431	2	US-08-480-515A-17	Sequence 17, Appl
31	402	100.0	431	2	US-08-459-129-2	Sequence 2, Appli
32	402	100.0	431	2	US-09-219-391-4	Sequence 4, Appli
33	402	100.0	431	2	US-08-469-411-6	Sequence 6, Appli
34	402	100.0	431	2	US-09-019-339B-2	Sequence 2, Appli
35	402	100.0	431	2	US-09-170-936-17	Sequence 17, Appl
36	402	100.0	431	2	US-08-402-542-2	Sequence 2, Appli
37	402	100.0	431	2	US-08-461-113-17	Sequence 17, Appl
38	402	100.0	431	2	US-08-828-281B-5	Sequence 5, Appli
39	402	100.0	431	2	US-09-887-901-2	Sequence 2, Appli
40	402	100.0	431	2	US-08-456-033-17	Sequence 17, Appl
41	402	100.0	431	2	US-08-643-321-16	Sequence 16, Appl
42	402	100.0	431	2	US-08-938-622-2	Sequence 2, Appli
43	402	100.0	431	2	US-09-148-925C-2	Sequence 2, Appli
44	402	100.0	431	2	US-08-957-425-2	Sequence 2, Appli
45	402	100.0	431	2	US-09-780-601A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
 US-07-841-646-2
 ; Sequence 2, Application US/07841646
 ; Patent No. 5266683
 ; GENERAL INFORMATION:
 ; APPLICANT: OPFERMANN, HERMANN
 ; APPLICANT: OZKAYNAK, ENGIN
 ; APPLICANT: KUBERASAMPATH, THANGAVEL
 ; APPLICANT: RUEGER, DAVID C.
 ; APPLICANT: PANG, ROY H.L.
 ; TITLE OF INVENTION: OSTEOGENIC DEVICES
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
 ; STREET: 53 STATE STREET
 ; CITY: BOSTON
 ; STATE: MASSACHUSETTS
 ; COUNTRY: U.S.A.

Search completed: January 5, 2006, 17:36:59
Job time : 53.4186 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:16:50 ; Search time 167.854 Seconds
(without alignments)
1000.675 Million cell updates/sec

Title: US-10-734-472-2_COPY_30_431
Perfect score: 402
Sequence: 1 DFSILDNEVHSSFIHRRLRSQ.....SSNVILKKYRNMVVRACGCH 402

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	402	100.0	427	4	US-10-367-094-171	Sequence 171, App	
2	402	100.0	427	4	US-10-367-094-175	Sequence 175, App	
3	402	100.0	431	2	US-08-822-186-2	Sequence 2, Appli	
4	402	100.0	431	2	US-08-937-755-2	Sequence 2, Appli	
5	402	100.0	431	2	US-08-957-425-2	Sequence 2, Appli	
6	402	100.0	431	2	US-08-260-675-17	Sequence 17, Appl	
7	402	100.0	431	3	US-09-045-331-2	Sequence 2, Appli	
8	402	100.0	431	3	US-09-828-607-2	Sequence 2, Appli	

9	402	100.0	431	3	US-09-887-901-2	Sequence 2, Appli
10	402	100.0	431	3	US-09-982-543A-10	Sequence 10, Appl
11	402	100.0	431	3	US-09-039-107-2	Sequence 2, Appli
12	402	100.0	431	3	US-09-798-518-1	Sequence 1, Appli
13	402	100.0	431	3	US-09-540-466-2	Sequence 2, Appli
14	402	100.0	431	3	US-09-423-943-2	Sequence 2, Appli
15	402	100.0	431	3	US-09-012-846-2	Sequence 2, Appli
16	402	100.0	431	3	US-09-960-789-1	Sequence 1, Appli
17	402	100.0	431	3	US-09-952-318A-17	Sequence 17, Appl
18	402	100.0	431	4	US-10-062-370-5	Sequence 5, Appli
19	402	100.0	431	4	US-10-083-825-2	Sequence 2, Appli
20	402	100.0	431	4	US-10-122-026-2	Sequence 2, Appli
21	402	100.0	431	4	US-10-272-503-2	Sequence 2, Appli
22	402	100.0	431	4	US-10-050-050-17	Sequence 17, Appl
23	402	100.0	431	4	US-10-286-152A-8	Sequence 8, Appli
24	402	100.0	431	4	US-10-301-822-10	Sequence 10, Appl
25	402	100.0	431	4	US-10-366-345-39	Sequence 39, Appl
26	402	100.0	431	4	US-10-321-799-2	Sequence 2, Appli
27	402	100.0	431	4	US-10-295-027-518	Sequence 518, App
28	402	100.0	431	4	US-10-295-027-787	Sequence 787, App
29	402	100.0	431	4	US-10-295-027-806	Sequence 806, App
30	402	100.0	431	4	US-10-295-027-843	Sequence 843, App
31	402	100.0	431	4	US-10-375-150-6	Sequence 6, Appli
32	402	100.0	431	4	US-10-173-999-58	Sequence 58, Appl
33	402	100.0	431	4	US-10-428-275-6	Sequence 6, Appli
34	402	100.0	431	4	US-10-428-997A-2	Sequence 2, Appli
35	402	100.0	431	4	US-10-302-812-28	Sequence 28, Appl
36	402	100.0	431	4	US-10-290-554-1	Sequence 1, Appli
37	402	100.0	431	4	US-10-753-916-2	Sequence 2, Appli
38	402	100.0	431	5	US-10-806-852-2	Sequence 2, Appli
39	402	100.0	431	5	US-10-995-979-2	Sequence 2, Appli
40	402	100.0	431	5	US-10-865-514-17	Sequence 17, Appl
41	402	100.0	431	5	US-10-492-380-8	Sequence 8, Appli
42	402	100.0	431	5	US-10-917-265-4	Sequence 4, Appli
43	402	100.0	431	5	US-10-968-791-5	Sequence 5, Appli
44	402	100.0	431	6	US-11-016-499-1	Sequence 1, Appli
45	402	100.0	431	6	US-11-021-902-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-367-094-171

; Sequence 171, Application US/10367094

; Publication No. US20040170982A1

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc Malandro

; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer

; FILE REFERENCE: 529452001500

; CURRENT APPLICATION NUMBER: US/10/367,094

; CURRENT FILING DATE: 2003-02-14

; NUMBER OF SEQ ID NOS: 203

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 171

; LENGTH: 427

Search completed: January 5, 2006, 17:43:40
Job time : 169.854 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:25:10 ; Search time 9.34884 Seconds
(without alignments)
364.935 Million cell updates/sec

Title: US-10-734-472-2_COPY_30_431
Perfect score: 402
Sequence: 1 DFSILDNEVHSSFIHRRRLRSQ.....SSNVILKKYRNMVVRACGCH 402

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 61072 seqs, 8486849 residues

Word size : 0

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	402	100.0	431	6	US-10-816-768-39	Sequence 39, Appl
2	402	100.0	431	6	US-10-650-326B-3	Sequence 3, Appli
3	402	100.0	431	7	US-11-051-568-2	Sequence 2, Appli
4	402	100.0	431	7	US-11-186-284-10	Sequence 10, Appl
5	334	83.1	408	7	US-11-051-568-15	Sequence 15, Appl
6	334	83.1	484	7	US-11-051-568-13	Sequence 13, Appl

7	259	64.4	317	7	US-11-051-568-11	Sequence 11, Appl
8	139	34.6	139	6	US-10-650-326B-1	Sequence 1, Appli
9	128	31.8	139	6	US-10-816-768-68	Sequence 68, Appl
10	106	26.4	117	6	US-10-816-768-69	Sequence 69, Appl
11	106	26.4	169	7	US-11-051-568-9	Sequence 9, Appli
12	102	25.4	102	6	US-10-816-768-55	Sequence 55, Appl
13	97	24.1	97	6	US-10-650-326B-2	Sequence 2, Appli
14	80	19.9	129	6	US-10-816-768-89	Sequence 89, Appl
15	71	17.7	139	6	US-10-650-326B-4	Sequence 4, Appli
16	71	17.7	430	6	US-10-650-326B-19	Sequence 19, Appl
17	71	17.7	430	7	US-11-051-568-25	Sequence 25, Appl
18	38	9.5	39	6	US-10-816-768-112	Sequence 112, App
19	35	8.7	46	6	US-10-816-768-91	Sequence 91, Appl
20	35	8.7	111	6	US-10-816-768-96	Sequence 96, Appl
21	30	7.5	39	6	US-10-816-768-121	Sequence 121, App
22	29	7.2	454	6	US-10-650-326B-15	Sequence 15, Appl
23	28	7.0	39	6	US-10-816-768-113	Sequence 113, App
24	28	7.0	39	6	US-10-816-768-114	Sequence 114, App
25	28	7.0	39	6	US-10-816-768-122	Sequence 122, App
26	28	7.0	39	6	US-10-816-768-123	Sequence 123, App
27	27	6.7	102	6	US-10-816-768-52	Sequence 52, Appl
28	26	6.5	35	6	US-10-816-768-5	Sequence 5, Appli
29	24	6.0	39	6	US-10-816-768-110	Sequence 110, App
30	24	6.0	43	6	US-10-816-768-104	Sequence 104, App
31	24	6.0	56	6	US-10-816-768-106	Sequence 106, App
32	22	5.5	64	6	US-10-816-768-108	Sequence 108, App
33	20	5.0	39	6	US-10-816-768-118	Sequence 118, App
34	19	4.7	35	6	US-10-816-768-6	Sequence 6, Appli
35	19	4.7	102	6	US-10-816-768-47	Sequence 47, Appl
36	19	4.7	438	6	US-10-650-326B-9	Sequence 9, Appli
37	19	4.7	513	6	US-10-650-326B-16	Sequence 16, Appl
38	19	4.7	513	7	US-11-000-463-816	Sequence 816, App
39	18	4.5	39	6	US-10-816-768-117	Sequence 117, App
40	18	4.5	39	6	US-10-816-768-119	Sequence 119, App
41	18	4.5	39	6	US-10-816-768-120	Sequence 120, App
42	17	4.2	39	6	US-10-816-768-115	Sequence 115, App
43	17	4.2	39	6	US-10-816-768-116	Sequence 116, App
44	15	3.7	15	6	US-10-816-768-102	Sequence 102, App
45	15	3.7	80	6	US-10-816-768-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1

US-10-816-768-39

; Sequence 39, Application US/10816768

; Publication No. US20050250936A1

; GENERAL INFORMATION:

; APPLICANT: Oppermann, Hermann

; APPLICANT: Tai, Mei-Sheng

; APPLICANT: McCartney, John

; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins

; FILE REFERENCE: STK-075

; CURRENT APPLICATION NUMBER: US/10/816,768

; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 124

Search completed: January 5, 2006, 17:44:07
Job time : 10.3488 secs

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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:13:39 ; Search time 34.8457 Seconds
(without alignments)
1110.013 Million cell updates/sec

Title: US-10-734-472-2_COPY_30_431
Perfect score: 402
Sequence: 1 DFSLDNEVHSSFIHRRRLRSQ.....SSNVILKKYRNMVVVRACGCH 402

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	402	100.0	431	1	BMHU7		bone morphogenetic
2	148	36.8	187	2	PN0496		bone morphogenetic
3	113	28.1	313	2	I51284		bone morphogenetic
4	71	17.7	430	2	JQ1184		osteogenic protein
5	32	8.0	426	2	JH0690		bone morphogenetic
6	29	7.2	452	2	I49542		bone morphogenetic
7	29	7.2	454	1	BMHU5		bone morphogenetic
8	19	4.7	207	2	S37618		vgr protein - rat
9	19	4.7	510	2	A54798		Vg-1-related prote
10	19	4.7	513	1	BMHU6		bone morphogenetic

11	14	3.5	34	2	A36626	osteogenic protein
12	14	3.5	455	2	A43918	TGF-beta-related p
13	13	3.2	402	2	A45056	osteogenic protein
14	13	3.2	461	2	S52408	SPDVR1 protein - s
15	10	2.5	351	2	A34201	bone morphogenetic
16	10	2.5	353	2	I50607	bone morphogenetic
17	10	2.5	393	2	S37073	bone morphogenetic
18	10	2.5	394	2	S45355	bone morphogenetic
19	10	2.5	396	1	BMHU2	bone morphogenetic
20	10	2.5	398	2	JH0688	bone morphogenetic
21	10	2.5	398	2	JH0687	bone morphogenetic
22	10	2.5	400	2	A49147	bone morphogenetic
23	10	2.5	401	2	JH0689	bone morphogenetic
24	10	2.5	405	2	I50608	bone morphogenetic
25	10	2.5	408	1	BMHU4	bone morphogenetic
26	10	2.5	408	2	S58791	bone morphogenetic
27	10	2.5	408	2	JH0801	bone morphogenetic
28	10	2.5	408	2	S38343	bone morphogenetic
29	10	2.5	420	2	I49541	bone morphogenetic
30	9	2.2	427	2	A40735	TGF beta homolog d
31	8	2.0	201	2	C95204	mechanosensitive i
32	8	2.0	201	2	C98071	hypothetical prote
33	8	2.0	202	2	AD1066	hypothetical prote
34	8	2.0	228	2	T39619	ubiquinol-cytochro
35	8	2.0	498	1	VGBEGX	secreted glycoprot
36	8	2.0	522	2	JA0072	hypothetical prote
37	8	2.0	717	2	H72208	conserved hypothet
38	8	2.0	777	2	T08659	ral guanine nucleo
39	7	1.7	83	2	E90706	hypothetical prote
40	7	1.7	83	2	H85556	hypothetical prote
41	7	1.7	124	2	AD0270	hypothetical prote
42	7	1.7	148	2	A81141	acyl CoA thioester
43	7	1.7	156	2	S67248	hypothetical prote
44	7	1.7	176	2	AC1207	hypothetical prote
45	7	1.7	208	2	H84233	membrane protein [

ALIGNMENTS

RESULT 1

BMHU7

bone morphogenetic protein 7 precursor - human

N;Alternate names: osteogenic protein 1

C;Species: Homo sapiens (man)

C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: C39263; S10529

R;Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozney, J.M.

Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990

A;Title: Identification of transforming growth factor beta family members present in bone-inductive protein purified from bovine bone.

A;Reference number: A39263; MUID:91088608; PMID:2263636

A;Accession: C39263

A;Molecule type: mRNA

A;Residues: 1-431 <CEL>

Search completed: January 5, 2006, 17:34:52
Job time : 34.8457 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:12:49 ; Search time 212.474 Seconds
(without alignments)
1334.860 Million cell updates/sec

Title: US-10-734-472-2_COPY_30_431
Perfect score: 402
Sequence: 1 DFSLDNEVHSSFIHRRQRSQ.....SSNVILKKYRNMVVRACGCH 402

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	402	100.0	431	1	BMP7_HUMAN	P18075 homo sapien
2	354	88.1	412	2	Q9BTB3_HUMAN	Q9btb3 homo sapien
3	148	36.8	187	1	BMP7_CANFA	P34819 canis famil
4	113	28.1	313	2	Q91403_CHICK	Q91403 gallus gall
5	113	28.1	398	2	Q9I8T6_CHICK	Q9i8t6 gallus gall
6	110	27.4	139	2	Q9H2W7_HUMAN	Q9h2w7 homo sapien
7	94	23.4	108	2	Q8MJC0_SHEEP	Q8mjc0 ovis aries
8	91	22.6	203	2	Q9CX35_MOUSE	Q9cx35 mus musculu
9	91	22.6	430	1	BMP7_MOUSE	P23359 mus musculu
10	84	20.9	365	2	Q5U916_PIG	Q5u916 sus scrofa
11	78	19.4	306	2	Q9R228_RAT	Q9r228 rattus norv
12	71	17.7	141	2	O88684_RAT	O88684 rattus norv

13	71	17.7	206	2	Q95L63_RABIT	Q95l63 oryctolagus
14	56	13.9	446	2	Q4S5J3_TETNG	Q4s5j3 tetraodon n
15	49	12.2	49	2	Q9MZL9_CANFA	Q9mzl9 canis famil
16	42	10.4	424	2	Q9YGH7_XENLA	Q9ygh7 xenopus lae
17	41	10.2	318	2	Q5BN41_ONCMY	Q5bn41 oncorhynchu
18	37	9.2	432	2	Q9PTF9_BRARE	Q9ptf9 brachydanio
19	33	8.2	426	2	Q6PF75_XENLA	Q6pf75 xenopus lae
20	32	8.0	426	1	BMP7_XENLA	P30886 xenopus lae
21	31	7.7	424	2	Q6P4J4_XENTR	Q6p4j4 xenopus tro
22	31	7.7	446	2	Q7T288_BRARE	Q7t288 brachydanio
23	30	7.5	254	2	Q4THC3_TETNG	Q4thc3 tetraodon n
24	29	7.2	154	2	Q4R5W6_MACFA	Q4r5w6 macaca fasc
25	29	7.2	450	2	Q4RQB0_TETNG	Q4rqb0 tetraodon n
26	29	7.2	452	1	BMP5_MOUSE	P49003 mus musculu
27	29	7.2	453	2	P87373_CHICK	P87373 gallus gall
28	29	7.2	454	1	BMP5_HUMAN	P22003 homo sapien
29	29	7.2	454	2	Q8CCE0_MOUSE	Q8cce0 mus musculu
30	28	7.0	425	2	Q4SS30_TETNG	Q4ss30 tetraodon n
31	23	5.7	424	2	Q6F2B8_XENTR	Q6f2b8 xenopus tro
32	19	4.7	207	1	BMP6_RAT	Q04906 rattus norv
33	19	4.7	428	2	Q4VBA3_HUMAN	Q4vba3 homo sapien
34	19	4.7	435	2	Q8BRW3_MOUSE	Q8brw3 mus musculu
35	19	4.7	441	2	Q52L10_XENLA	Q52l10 xenopus lae
36	19	4.7	483	2	Q4JCQ2_HUMAN	Q4j cq2 homo sapien
37	19	4.7	506	2	Q811S4_RAT	Q811s4 rattus norv
38	19	4.7	510	1	BMP6_MOUSE	P20722 mus musculu
39	19	4.7	513	1	BMP6_HUMAN	P22004 homo sapien
40	19	4.7	513	2	Q5TCP3_HUMAN	Q5tcp3 homo sapien
41	18	4.5	124	2	Q9I8Q8_CHICK	Q9i8q8 gallus gall
42	15	3.7	112	2	Q4SYC6_TETNG	Q4syc6 tetraodon n
43	14	3.5	34	2	Q7M302_BOVIN	Q7m302 bos taurus
44	14	3.5	100	2	Q8MJC1_SHEEP	Q8mjcl1 ovis aries
45	14	3.5	417	2	Q5CZV5_BRARE	Q5czv5 brachydanio

ALIGNMENTS

RESULT 1

BMP7_HUMAN

ID BMP7_HUMAN STANDARD; PRT; 431 AA.
 AC P18075; Q9H512; Q9NTQ7;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Bone morphogenetic protein 7 precursor (BMP-7) (Osteogenic protein 1)
 DE (OP-1) (Eptotermin alfa).
 GN Name=BMP7; Synonyms=OP1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=90291971; PubMed=2357959;

OM protein - protein search, using sw model

Run on: January 5, 2006, 17:12:04 ; Search time 52.2939 Seconds
(without alignments)
857.015 Million cell updates/sec

Title: US-10-734-472-2_COPY_330_431
Perfect score: 102
Sequence: 1 CKKHELYVSFRDLGWQDWII.....SSNVILKKYRNMVVRACGCH 102

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	102	100.0	102	1 AAP95682	Aap95682 Human ost
2	102	100.0	102	2 AAR53360	Aar53360 Osteogeni
3	102	100.0	102	2 AAW36889	Aaw36889 Human ost
4	102	100.0	102	2 AAW36872	Aaw36872 Human ost
5	102	100.0	102	2 AAY16708	Aay16708 W09914235
6	102	100.0	102	2 AAW89697	Aaw89697 Human ost
7	102	100.0	102	2 AAW95443	Aaw95443 Conserved
8	102	100.0	102	3 AAY92569	Aay92569 OP-1 fing

9	102	100.0	102	3	AAB09534	Aab09534	Human OP-
10	102	100.0	102	3	AAB02800	Aab02800	Human OP-
11	102	100.0	102	4	AAU10599	Aau10599	Human ost
12	102	100.0	102	5	ABB76281	Abb76281	Mature hu
13	102	100.0	102	8	ADG14142	Adg14142	Human ost
14	102	100.0	102	8	ADO36196	Ado36196	Transform
15	102	100.0	102	9	ADZ84363	Adz84363	Human OP-
16	102	100.0	103	8	ADV86574	Adv86574	Bone morp
17	102	100.0	104	8	ADT04078	Adt04078	Human bon
18	102	100.0	110	8	ADV86573	Adv86573	Bone morp
19	102	100.0	114	2	AAR53361	Aar53361	N-termina
20	102	100.0	114	2	AAW95454	Aaw95454	N-termina
21	102	100.0	116	2	AAR53362	Aar53362	N-termina
22	102	100.0	116	2	AAW95453	Aaw95453	N-termina
23	102	100.0	117	2	AAR53363	Aar53363	N-termina
24	102	100.0	117	2	AAW95452	Aaw95452	N-termina
25	102	100.0	119	2	AAR53364	Aar53364	N-termina
26	102	100.0	119	2	AAW95451	Aaw95451	N-termina
27	102	100.0	119	6	ABG76026	Abg76026	Human OP-
28	102	100.0	131	5	ABB07963	Abb07963	Human BMP
29	102	100.0	132	2	AAR53365	Aar53365	N-termina
30	102	100.0	132	2	AAW95450	Aaw95450	N-termina
31	102	100.0	138	2	AAV08297	Aay08297	Human gro
32	102	100.0	139	2	AAR27285	Aar27285	Mature hu
33	102	100.0	139	2	AAR53366	Aar53366	N-termina
34	102	100.0	139	2	AAR33921	Aar33921	Morphogen
35	102	100.0	139	2	AAR33398	Aar33398	Human mat
36	102	100.0	139	2	AAR46724	Aar46724	Human mat
37	102	100.0	139	2	AAR60967	Aar60967	Mature hu
38	102	100.0	139	2	AAR71974	Aar71974	BMP-7. 10
39	102	100.0	139	2	AAW00222	Aaw00222	Mouse mat
40	102	100.0	139	2	AAW00221	Aaw00221	Human mat
41	102	100.0	139	2	AAW40180	Aaw40180	Human hOP
42	102	100.0	139	2	AAW36871	Aaw36871	Mature pr
43	102	100.0	139	2	AAW54064	Aaw54064	Bone morp
44	102	100.0	139	2	AAW84215	Aaw84215	Bone morp
45	102	100.0	139	2	AAW95449	Aaw95449	Mature hu

ALIGNMENTS

RESULT 1

AAP95682

ID AAP95682 standard; protein; 102 AA.

XX

AC AAP95682;

XX

DT 25-MAR-2003 (revised)

DT 21-AUG-1990 (first entry)

XX

DE Human osteogenic protein 1(OP1-II) for osteogenic device.

XX

KW Osteogenic device; osteogenic protein; endochronal bone;

KW biodegradable matrix.

XX

OS Synthetic.

Search completed: January 5, 2006, 17:24:55
Job time : 54.2939 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:16:35 ; Search time 13.0465 Seconds
(without alignments)
646.373 Million cell updates/sec

Title: US-10-734-472-2_COPY_330_431
Perfect score: 102
Sequence: 1 CKKHELYVSFRDLGWQDWII.....SSNVILKKYRNMVVRACGCH 102

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	102	100.0	102	1	US-08-335-583C-47	Sequence 47, Appl
2	102	100.0	102	1	US-08-288-508C-18	Sequence 18, Appl
3	102	100.0	102	2	US-08-478-097A-16	Sequence 16, Appl
4	102	100.0	102	2	US-08-289-222E-27	Sequence 27, Appl
5	102	100.0	102	2	US-09-054-526B-27	Sequence 27, Appl
6	102	100.0	102	2	US-08-931-858E-161	Sequence 161, App
7	102	100.0	102	2	US-08-981-739-161	Sequence 161, App
8	102	100.0	102	2	US-08-786-284A-1	Sequence 1, Appli

9	102	100.0	102	2	US-09-128-026-161	Sequence 161, App
10	102	100.0	102	2	US-09-496-398-16	Sequence 16, Appl
11	102	100.0	102	2	US-09-220-616-161	Sequence 161, App
12	102	100.0	102	2	US-09-374-958C-55	Sequence 55, Appl
13	102	100.0	102	2	US-09-220-527-161	Sequence 161, App
14	102	100.0	102	2	US-09-220-407-161	Sequence 161, App
15	102	100.0	102	2	US-09-386-450D-18	Sequence 18, Appl
16	102	100.0	102	2	US-09-374-936-55	Sequence 55, Appl
17	102	100.0	104	1	US-07-764-731B-8	Sequence 8, Appli
18	102	100.0	118	1	US-08-481-377-12	Sequence 12, Appl
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20	102	100.0	118	2	US-09-153-733A-12	Sequence 12, Appl
21	102	100.0	118	2	US-08-946-092A-10	Sequence 10, Appl
22	102	100.0	118	2	US-09-172-062-10	Sequence 10, Appl
23	102	100.0	118	2	US-09-301-520D-10	Sequence 10, Appl
24	102	100.0	118	2	US-09-389-705-12	Sequence 12, Appl
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33	102	100.0	119	2	US-08-624-635-13	Sequence 13, Appl
34	102	100.0	119	2	US-09-145-060-18	Sequence 18, Appl
35	102	100.0	119	2	US-09-378-238-26	Sequence 26, Appl
36	102	100.0	119	2	US-09-629-938-22	Sequence 22, Appl
37	102	100.0	119	2	US-09-686-344-40	Sequence 40, Appl
38	102	100.0	119	2	US-09-412-791D-12	Sequence 12, Appl
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42	102	100.0	119	4	PCT-US94-07799-12	Sequence 12, Appl
43	102	100.0	139	1	US-07-718-274A-2	Sequence 2, Appli
44	102	100.0	139	1	US-08-163-877-10	Sequence 10, Appl
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ALIGNMENTS

RESULT 1

US-08-335-583C-47

; Sequence 47, Application US/08335583C

; Patent No. 5693779

; GENERAL INFORMATION:

; APPLICANT: Moos Jr., Malcolm

; APPLICANT: Wang, Shouwan

; APPLICANT: Krinks, Marie

; TITLE OF INVENTION: PRODUCTION AND USE OF

; TITLE OF INVENTION: ANTI-DORSALIZING MORPHOGENETIC PROTEIN

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson and Bear

; STREET: 620 Newport Center Drive 16th Floor

; CITY: Newport Beach

Search completed: January 5, 2006, 17:36:55
Job time : 14.0465 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2006, 17:16:50 ; Search time 42.5899 Seconds
(without alignments)
1000.675 Million cell updates/sec

Title: US-10-734-472-2_COPY_330_431
Perfect score: 102
Sequence: 1 CKKHELYVSFRDLGWQDWII.....SSNVILKKYRNMVVRACGCH 102

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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5	102	100.0	102	6	US-11-105-344-27	Sequence 27, Appl	
6	102	100.0	102	6	US-11-037-782-161	Sequence 161, App	
7	102	100.0	104	5	US-10-811-492-2	Sequence 2, Appli	
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14	102	100.0	119	3	US-09-813-459-13	Sequence 13, Appl
15	102	100.0	119	3	US-09-859-211-40	Sequence 40, Appl
16	102	100.0	119	3	US-09-880-708-18	Sequence 18, Appl
17	102	100.0	119	3	US-09-872-856-40	Sequence 40, Appl
18	102	100.0	119	4	US-10-335-483-22	Sequence 22, Appl
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26	102	100.0	139	4	US-10-050-050-5	Sequence 5, Appli
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43	102	100.0	195	3	US-09-765-527-263	Sequence 263, App
44	102	100.0	317	2	US-08-957-425-11	Sequence 11, Appl
45	102	100.0	317	4	US-10-321-799-11	Sequence 11, Appl

ALIGNMENTS

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US-09-791-946-1

; Sequence 1, Application US/09791946

; Patent No. US20020028453A1

; GENERAL INFORMATION:

; APPLICANT: KECK, PETER

; GRIFFITH, DIANA L

; CARLSON, WILLIAM D

; RUEGER, DAVID C

; SAMPATH, KUBER T

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
MORPHOGEN ANALOGS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,

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Run on: January 5, 2006, 17:25:10 ; Search time 2.37209 Seconds
(without alignments)
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Gapop 60.0 , Gapext 60.0

Searched: 61072 seqs, 8486849 residues

Word size : 0

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Post-processing: Listing first 45 summaries

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SUMMARIES

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6	102	100.0	431	6	US-10-816-768-39	Sequence 39, Appl	
7	102	100.0	431	6	US-10-650-326B-3	Sequence 3, Appli	
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10	102	100.0	484	7	US-11-051-568-13	Sequence 13, Appl	
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12	91	89.2	139	6	US-10-816-768-68	Sequence 68, Appl	
13	72	70.6	129	6	US-10-816-768-89	Sequence 89, Appl	

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20	28	27.5	39	6	US-10-816-768-114	Sequence 114, App
21	28	27.5	39	6	US-10-816-768-122	Sequence 122, App
22	28	27.5	39	6	US-10-816-768-123	Sequence 123, App
23	27	26.5	102	6	US-10-816-768-52	Sequence 52, Appl
24	27	26.5	454	6	US-10-650-326B-15	Sequence 15, Appl
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29	19	18.6	102	6	US-10-816-768-47	Sequence 47, Appl
30	19	18.6	438	6	US-10-650-326B-9	Sequence 9, Appli
31	19	18.6	513	6	US-10-650-326B-16	Sequence 16, Appl
32	19	18.6	513	7	US-11-000-463-816	Sequence 816, App
33	18	17.6	39	6	US-10-816-768-117	Sequence 117, App
34	18	17.6	39	6	US-10-816-768-119	Sequence 119, App
35	18	17.6	39	6	US-10-816-768-120	Sequence 120, App
36	17	16.7	39	6	US-10-816-768-115	Sequence 115, App
37	17	16.7	39	6	US-10-816-768-116	Sequence 116, App
38	15	14.7	102	6	US-10-816-768-53	Sequence 53, Appl
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42	12	11.8	102	6	US-10-816-768-57	Sequence 57, Appl
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44	12	11.8	399	6	US-10-650-326B-23	Sequence 23, Appl
45	12	11.8	399	7	US-11-051-568-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-10-816-768-55

; Sequence 55, Application US/10816768

; Publication No. US20050250936A1

; GENERAL INFORMATION:

; APPLICANT: Oppermann, Hermann

; APPLICANT: Tai, Mei-Sheng

; APPLICANT: McCartney, John

; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins

; FILE REFERENCE: STK-075

; CURRENT APPLICATION NUMBER: US/10/816,768

; CURRENT FILING DATE: 2004-04-02

; NUMBER OF SEQ ID NOS: 124

; SOFTWARE: PatentIn version 2.0

; SEQ ID NO 55

; LENGTH: 102

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: OP-1

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(without alignments)
1110.013 Million cell updates/sec

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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	59	57.8	430	2	JQ1184	osteogenic protein
4	32	31.4	426	2	JH0690	bone morphogenetic
5	27	26.5	452	2	I49542	bone morphogenetic
6	27	26.5	454	1	BMHU5	bone morphogenetic
7	19	18.6	207	2	S37618	vgr protein - rat
8	19	18.6	510	2	A54798	Vg-1-related prote
9	19	18.6	513	1	BMHU6	bone morphogenetic
10	14	13.7	34	2	A36626	osteogenic protein
11	14	13.7	455	2	A43918	TGF-beta-related p
12	13	12.7	461	2	S52408	SPDVR1 protein - s
13	10	9.8	351	2	A34201	bone morphogenetic

14	10	9.8	353	2	I50607	bone morphogenetic
15	10	9.8	393	2	S37073	bone morphogenetic
16	10	9.8	394	2	S45355	bone morphogenetic
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18	10	9.8	398	2	JH0688	bone morphogenetic
19	10	9.8	398	2	JH0687	bone morphogenetic
20	10	9.8	400	2	A49147	bone morphogenetic
21	10	9.8	401	2	JH0689	bone morphogenetic
22	10	9.8	405	2	I50608	bone morphogenetic
23	10	9.8	408	1	BMHU4	bone morphogenetic
24	10	9.8	408	2	S58791	bone morphogenetic
25	10	9.8	408	2	JH0801	bone morphogenetic
26	10	9.8	408	2	S38343	bone morphogenetic
27	10	9.8	420	2	I49541	bone morphogenetic
28	9	8.8	427	2	A40735	TGF beta homolog d
29	8	7.8	402	2	A45056	osteogenic protein
30	7	6.9	124	2	AD0270	hypothetical prote
31	7	6.9	347	2	T50990	hypothetical prote
32	7	6.9	365	2	T43286	cet-1 protein - Ca
33	7	6.9	373	2	A41918	transforming growt
34	7	6.9	379	2	T29518	hypothetical prote
35	7	6.9	464	2	T50955	hypothetical prote
36	7	6.9	475	2	S49886	probable membrane
37	7	6.9	496	2	G96516	hypothetical prote
38	7	6.9	571	2	E90027	urease alpha subun
39	7	6.9	2206	1	GNNY21	genome polyprotein
40	6	5.9	33	2	B36193	inhibin beta-A cha
41	6	5.9	47	2	B36626	osteogenic protein
42	6	5.9	48	2	F64086	glycerol-3-phospha
43	6	5.9	67	2	A69342	hypothetical prote
44	6	5.9	79	2	S21473	transforming growt
45	6	5.9	92	2	H87605	hypothetical prote

ALIGNMENTS

RESULT 1

I51284

bone morphogenetic protein-7 - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004

C;Accession: I51284

R;Houston, B.; Thorp, B.H.; Burt, D.W.

J. Mol. Endocrinol. 13, 289-301, 1994

A;Title: Molecular cloning and expression of bone morphogenetic protein-7 in the chick epiphyseal growth plate.

A;Reference number: I51284; MUID:95200473; PMID:7893347

A;Accession: I51284

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-313 <HOU>

A;Cross-references: UNIPROT:Q91403; UNIPARC:UPI00000FBD3B; GB:S77477;

NID:g957233; PIDN:AAB33846.1; PID:g957234

C;Superfamily: inhibin

Query Match

100.0%; Score 102; DB 2; Length 313;

A;Cross-references: UNIPROT:Q90751; UNIPARC:UPI0000126A1F; EMBL:X75914;
NID:g472927; PIDN:CAA53513.1; PID:g472928
C;Genetics:
A;Gene: Bmp-2
C;Superfamily: inhibin

Query Match 9.8%; Score 10; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 TNHAIVQTLV 54
|||
Db 297 TNHAIVQTLV 306

RESULT 15

S37073

bone morphogenetic protein 2 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: S37073

R;Feng, J.Q.; Chen, D.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.
submitted to the EMBL Data Library, September 1993

A;Description: cDNA sequence of fetal rat calvarial osteoblast bone
morphogenetic protein 2.

A;Reference number: S37073

A;Accession: S37073

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-393 <FEN>

A;Cross-references: UNIPROT:P49001; UNIPARC:UPI0000126A23; EMBL:Z25868;
NID:g397950; PIDN:CAA81088.1; PID:g397951

C;Superfamily: inhibin

Query Match 9.8%; Score 10; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 TNHAIVQTLV 54
|||
Db 337 TNHAIVQTLV 346